

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:35:33 ; Search time 5937.36 Seconds
(without alignments)
12661.132 Million cell updates/sec

Title: US-09-856-681-1

Sequence: 3093
1 atcaggtcagaaacctgtc.....ccaatgatcgtctacataa 3093

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrl:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3089.8	99.9	6875	11 BC032619	Homo sapi
2	1439.4	46.5	3226	11 AK042751	Mus muscu
3	1437.6	46.5	3329	11 AK082711	Mus muscu
4	1065.8	34.5	2411	14 CB605722	AMGNNUC:M

5	899.4	29.1	1030	12 BM450002	BM450002 AGENCOURT
6	895	29.0	1183	12 BM546059	BM546059 AGENCOURT
7	828.2	26.8	868	9 A0140366	A0140366 AGENCOURT
8	813.8	26.3	891	13 B0186963	B0186963 AGENCOURT
9	784.4	25.4	887	12 BG769297	BG769297 AGENCOURT
10	783.4	25.3	1201	9 AL543344	AL543344 AGENCOURT
11	779.4	25.2	848	13 B0678536	B0678536 AGENCOURT
12	772.4	25.0	883	13 B0172225	B0172225 AGENCOURT
13	770	24.9	864	13 B0440312	B0440312 AGENCOURT
14	767.4	24.8	874	13 B0838082	B0838082 AGENCOURT
15	760.6	24.6	890	13 B0683009	B0683009 AGENCOURT
16	757.4	24.5	953	13 B0854884	B0854884 AGENCOURT
17	734	23.7	952	13 B0855855	B0855855 AGENCOURT
18	713.8	23.1	835	10 B0477592	B0477592 AGENCOURT
19	682.2	22.1	4374	11 AK031307	AK031307 Mus muscu
20	681.8	22.0	3921	11 AK084922	AK084922 Mus muscu
21	680.2	22.0	4476	11 AK052232	AK052232 Mus muscu
22	670.2	21.7	716	10 BF970807	BF970807 602271438
23	667	21.6	890	13 B0856543	B0856543 AGENCOURT
24	664.8	21.5	736	10 BE277845	BE277845 AGENCOURT
25	660.4	21.4	794	10 AW954605	AW954605 EST36675
26	656.2	21.2	823	10 BG327694	BG327694 602426630
27	645.8	20.9	651	9 AL602452	AL602452 DKEZP686M
28	636.6	20.6	643	10 BE408781	BE408781 601303483
29	631.8	20.4	685	10 BE265000	BE265000 601193829
30	629.8	20.4	703	10 BE384511	BE384511 601277886
31	615.2	19.9	926	10 BG326467	BG326467 602425312
32	614.4	19.9	746	13 B0770491	B0770491 UI-M-FIO-
33	614.4	19.9	795	14 CB245479	CB245479 UI-M-FIO-
34	612.2	19.8	772	13 B0425051	B0425051 AGENCOURT
35	611.8	19.8	895	12 B0819955	B0819955 603035314
36	608.8	19.7	777	13 B0708655	B0708655 UI-M-FIO-
37	604.4	19.5	771	14 CA513024	CA513024 UI-M-FIO-
38	589.6	19.1	829	12 B1824613	B1824613 603033546
39	589.2	19.0	690	10 BG333712	BG333712 602460715
40	588.8	19.0	592	14 CA337090	CA337090 MISC.1099
41	588.8	19.0	884	10 B0728944	B0728944 601562382
42	578	18.7	603	10 BG334875	BG334875 602460878
43	576.8	18.6	852	10 BF306161	BF306161 601893009
44	573	18.5	713	10 BE389749	BE389749 601282916
45	570.4	18.4	612	10 BG327283	BG327283 602426042

ALIGNMENTS

RESULT 1
BC032619 6875 bp mRNA linear HTC 04-MAR-2003
LOCUS Homo sapiens, similar to sema domain, transmembrane domain (TM) and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:578066, mRNA.
DEFINITION BC032619
ACCESSION BC032619.1 GI:22749800
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: ATCC/DOCI/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland:
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgenhgti.nih.gov

Ahler, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lurie, P., Legaspi, R.,
Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Staudt, P.S., Thomas, P.J., Touchman, J.W.,
Tureoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILN at: <http://image.llnl.gov>
Series: IRK Plate: 69 Row: 0 Column: 4

This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 11991659
This clone has the following problem: retained intron.

FEATURES

source

1. 6875

/organism="Homo sapiens"

/mol_type="mrna"

/db_xref="taxon:9606"

/clone="IMAGE:5578066"

/tissue_type="Skin, melanotic melanoma."

/clone_lib="NIH_MGC_72"

/lab_host="DH10B"

/note="Vector: pCMV-Sport6"

BASE COUNT 1784 a 1795 c 1592 g 1704 t

ORIGIN

Query Match

Best Local Similarity

Matches 3091; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

99.9%; Score 3089.8; DB 11; Length 6875;

Pred No. 0;

Matches 3091; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAGGTCAGAAAGCCCTGCTGCTATATTTTACACAGCTGCTACCTTCTGGGGGTGTTTC 60
792 ATGAGGTCAGAAAGCCCTGCTGCTATATTTTACACAGCTGCTACCTTCTGGGGGTGTTTC 851
61 CCAGAGATTTGAGGCAATCAAGTATTTTGGCATGGCACTATACAAAGATATCCGGTG 120
852 CCAGAGATTTGAGGCAATCAAGTATTTTGGCATGGCACTATACAAAGATATCCGGTG 911
121 TTGTGGGCCACAAAGCCAGAGAGCAACACACAGAGGAGGCTGGCATCCAGATG 180
912 TTGTGGGCCACAAAGCCAGAGAGCAACACACAGAGGAGGCTGGCATCCAGATG 971
181 ATTATGATCATGAACGGAACCCCTACATTTGCTGAGGACCATATTTACTGTTGAT 240
972 ATTATGATCATGAACGGAACCCCTACATTTGCTGAGGACCATATTTACTGTTGAT 1031
241 ATGAGCATCATCAACAGGAAATTTTATTAGCAAAAACCTGACATGAAATCTAGA 300
1032 ATGAGCATCATCAACAGGAAATTTTATTAGCAAAAACCTGACATGAAATCTAGA 1091
301 CAGGCGATGTAGACATCATGAGATGAAGGAAACATATAGATGAGTGCACAACTTT 360
1092 CAGGCGATGTAGACATCATGAGATGAAGGAAACATATAGATGAGTGCACAACTTT 1151
361 ATTAAGTTCTTCTAAAGAAAAAGATGATGATTTGCTGTTGGAATTAAGCTTTC 420
1152 ATTAAGTTCTTCTAAAGAAAAAGATGATGATTTGCTGTTGGAATTAAGCTTTC 1211
421 AACCTGCTGAGAAACATATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
1212 AACCTGCTGAGAAACATATAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1271
481 GGAATGGCAGATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
1272 GGAATGGCAGATGGCCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1331
541 AAATATATCTAGCCACAGTACTGATCTTCTGATGATGATGATGATGATGATGATGATGAT 600

1332 AAATATATCTAGCCACAGTACTGATCTTCTGATGATGATGATGATGATGATGATGATGAT 1391
601 CTGAGAAAGCCCTACCTCGGAGCCGTAGACAGATTCAAATGGTGAAGAACCA 660
1392 CTGAGAAAGCCCTACCTCGGAGCCGTAGACAGATTCAAATGGTGAAGAACCA 1451
661 TACTTTGTCAGCCGTGATTAAGAGATTAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
1452 TACTTTGTCAGCCGTGATTAAGAGATTAATATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1511
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781 GATATGAGAGATCTCAAAAGATCCGAGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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1632 TTGAGCTGCTAGTCTGAGAGATCTGATTTTATTTTCAATTTCTCCAGAGATTAACA 1691
901 GATGATATGATCAACAGAGAGAGATGTTTCTCTGCAACGTTTCTACACCTTATAC 960
1692 GATGATATGATCAACAGAGAGATGTTTCTCTGCAACGTTTCTACACCTTATAC 1751
961 AGCATCCCTGGGCTGCTGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1020
1752 AGCATCCCTGGGCTGCTGAGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1811
1021 GGAAGATTTAAGAGAAAGAGATCTGATTTCCATCCAGTGGACACAGTCTGATGAGCA 1080
1812 GGAAGATTTAAGAGAAAGAGATCTGATTTCCATCCAGTGGACACAGTCTGATGAGCA 1871
1081 GTTCCCTAAGCCAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
1872 GTTCCCTAAGCCAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1931
1141 TCCATGATTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1932 TCCATGATTTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991
1201 GGAAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1992 GGAAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
1261 ACCAAATTTGAGTGAACAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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2112 GATCAGAGAGAGGAAATCTTGAAGTTTGGCCAGAAATAGGAAATAGTGGTTCCTA 2171
1381 AATGACAGCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
2172 AATGACAGCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2231
1441 GGAAGTGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
2232 GGAAGTGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2291
1501 GTTGGTCTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
2292 GTTGGTCTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2351
1561 TGTAAAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
2352 TGTAAAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2411
1621 GCTGACAGCATTTTATCAACCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
2412 GCTGACAGCATTTTATCAACCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2471

QY 1681 AATACAGATGTCCTGGGGGAGCTGTCAAAATCTCTTGTGGCACTGAATGGGATTCACAG 1740
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 QY 1741 TCCCTTGTGGGAGCAACACATCAGATTCGACGGCTCAAGAGGGGTATGATGTAGG 1800
 DB 2532 TCCCTTGTGGGAGCAACACATCAGATTCGACGGCTCAAGAGGGGTATGATGTAGG 2591
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 DB 2592 GGAGAAATGCTGGAGTGAAGATCTGCTTGAATCACTGACAGCAACACATCTTTGGGG 2651
 QY 1861 GGAGTGTCTTCCCATATCACCACAGAGAGAGAGATTCGGGAAAGTTACCTCAAA 1920
 DB 2652 GGAGTGTCTTCCCATATCACCACAGAGAGAGATTCGGGAAAGTTACCTCAAA 2711
 QY 1921 GGCCACGACAGCTGGTTCCTGCTCACTCCCTCTTGGCCATTCAGTCACTCTGCTTCTG 1980
 DB 2712 GGCCACGACAGCTGGTTCCTGCTCACTCCCTCTTGGCCATTCAGTCACTCTGCTTCTG 2771
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 DB 2832 GTGGCTGTGTGACAGCAGAGAGAGAGAGTCAACCCGCTCTGCTGTGATCATCGCGCAAG 2891
 QY 2101 AGCTTACACCAAGCTCAGCGGCTCTTGTGGGAGACTCAATCCAAAGACCCAAAGCCGAG 2160
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 QY 2161 GCCATCTCAGCCCACTCATGACAGAGAGAGAGTCAACCCGCTCTGCTGTGATCATCGCGCAAG 2220
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 DB 3852 ACATCCATGAGAGAGAGAGTCAACCCGCTCTGCTGTGATCATCGCGCAAG 3884

RESULT 2
 AK042751
 LOCUS
 DEFINITION
 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A730020P05 product:sema domain,
 transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A,
 full insert sequence.

AK042751
 AK042751.1 GI:26335300
 HTG: CAP trapper.
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 PUBMED

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 AUTHORS
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 4
 11076861

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
 Aizawa, K., Hara, A., Fukunishi, Y., Kono, H., Adachi, T., Fukuda, S.,
 Aizawa, K., Iizawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Imanaka, I.,
 Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
 Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
 Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,

Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balatelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinci, P., de Bernaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustlincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sakaki, H., Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weltz, C., Whitaker, C., Wilming, L., Wyszynski, B., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S., and Hayashizaki, Y.

TITLE
Functional annotation of a full-length mouse cDNA collection

JOURNAL
Nature 409 (6821), 685-690 (2001)

MEDLINE
21085660

PUBMED
11217851

REFERENCE
5

AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
Nature 420, 563-573 (2002)

REFERENCE
6 (bases 1 to 3226)

AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE
Direct Submission

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

SOURCE
1. 3226
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM:DB:A730020P05"
/db_xref="taxon:10090"
/clone="A730020P05"
/tissue_type="cerebellum"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="7 days neonate"
671..2488

CDS
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ORGANISM	
REFERENCE	
AUTHORS	1
Carninci, P. and Hayashizaki, Y.	
JOURNAL	High efficiency full-length cDNA cloning
TITLE	with Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
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REFERENCE	
AUTHORS	2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
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TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
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AUTHORS	3
Shibata, K., Itch, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,	
Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itch, M.,	
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Ishimoto, R., Matsuno, H., Sekiguchi, S., Ikegami, T., Kashiwagi, K.,	
Fujiwara, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,	
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TITLE	RIKEN integrated sequence analysis (RISA) system-384-format
JOURNAL	sequencing pipeline with 384 multiplexed sequencer
MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	20530913
REFERENCE	
AUTHORS	4
Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y.,	
Arakawa, T., Hata, A., Fukunishi, Y., Kono, H., Aichi, J., Fukuda, S.,	
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Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,	
Etlinger, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,	
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,	
Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilmink, L.,	
Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kotsuki, S.	
and Hayashizaki, Y.	
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	
AUTHORS	5
The RIKEN Consortium and the RIKEN Genome Exploration Research	
Group Phase I & II Team.	
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (phases 1 to 3329)
Aichi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,	
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,	
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,	
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TITLE
JOURNAL

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/
URL: http://phantom.gsc.riken.go.jp/.

FEATURES

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Matches 1551; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 2411)
 AUTHORS Amgen EST Program.
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00075 row: d column: 4.

FEATURES
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 Db 506 CGGATCATGCTGTATTTGTGTGTGATCATGCGGCAAGACGAGGTGTGTGTGACAG 565
 QY 2058 CAAAGAGAGAGCTCACCCACTGCGCGCGGGGCTCCATGAGACGCTCACCAAGCTGAG 2117
 Db 566 CAAAGAGAGAGCTCACCCACTGCGCGCGGGGCTCCATGAGACGCTCACCAAGCTGAG 625
 QY 2118 CGGCTCTTTGGGAGACACTCAATCCAAAGACCCAAAGCGGACATCTCTACAGCT 2177
 Db 626 TGGCTCTTTGGGAGACACTCAATCCAAAGACCCAAAGCGGACATCTCTACAGCT 685
 QY 2178 CATGACACAGCGAAGCTCGGCACTCCCGGCAACAGGCGCAAGATGCTCATTAAGCAGA 2237
 Db 686 CATGACACAGCGAAGCTCGGCACTCCCGGCAACAGGCGCAAGATGCTCATTAAGCAGA 745
 QY 2238 CAGACACACCTGAGCTGACGCTCCCTCCACCCCAAGAGTCAACCCCAAGCTGACAGA 2297
 Db 746 CAGACATCACTTAAGCTCAACCGGCTCCACCCCAAGAGTCAACCCCAAGCTGACAGA 805
 QY 2298 GAAGCGGAGAGCGGCGGCGGAGCGGAGTGGGAGAGAGACAGAAACCTCATCATTC 2357
 Db 806 GAAGCGGAGAGCGGCGGCGGAGTGGGAGAGAGACAGAAACCTCATCATTC 865
 QY 2358 CTGCAAAAGAGATGCGCCCATGAGGCTCCCTCTGTATTCACAGGACCTGCCCCGCG 2417
 Db 866 CTGCAAAAGAGAT----- 880
 QY 2418 GGGCTCCCAAGCACATCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2477
 Db 881 -GGCTCCCAAGCACATCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 939
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 Db 940 GCATGATGATGAGGACCCCAAAATGAGAGGAGTGTGTGTGTGTGTGTGTGTGTGT 999
 QY 2535 CCAAGGCGCCACACTGAGATATTAAGACCATTAAGGAACATCTGAGACAGAAAGTCCCAA 2594

100

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
QY	1088	ACCCAGGCGCAGGTGCGTGTGGCTCATCTCTTGGAAGATATCAACCTCCATG	B0186963	5'	nrna	sequence.	Homo sapiens	EST.	1	(bases 1 to 891)	NIH-MGC	http://mgc.nci.nih.gov/.
Db	721	ACCCAGGCGCAGGTGCGTGTGGCTCATCTCTTGGAAGATATCAACCTCCATG	B0186963	1	GI:22700947	EST.	Homo sapiens	EST.	1	(bases 1 to 891)	NIH-MGC	http://mgc.nci.nih.gov/.
QY	1148	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
QY	1208	CCTTCATCTTCAACAGGCGCATGCTTCCCTGA	B0186963	1	GI:22700947	EST.	Homo sapiens	EST.	1	(bases 1 to 891)	NIH-MGC	http://mgc.nci.nih.gov/.
Db	839	CCTTCATCTTCAACAGGCGCATGCTTCCCTGA	B0186963	1	GI:22700947	EST.	Homo sapiens	EST.	1	(bases 1 to 891)	NIH-MGC	http://mgc.nci.nih.gov/.
QY	1448	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
QY	1448	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
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Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
QY	1448	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
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Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
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Db	781	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
QY	1448	ACTTCCCTGATGATATACCTTGACCTTCATCAAGACGACCCGCTCATGATGATGAGCAGTGC	B0186963	891	bp	nrna	linear	EST	04-SEP-2002			
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Db      662 CATGAGAGACATCTCAGCAGCAAGAGTCCCAACCATGGGGGTGAACCTTTGGAGAAC 721
QY      2621 TGGACAGCGCTGCCCCCAAGTTCACACGCGGAGCGCTCCCTGGGTCCCGGGA -GC 2678
Db      722 TGGACAGCGCTGCCCCCAAGTTCACACGCGGAGCGCTCCCTGGGTCCCGGGA 781
QY      2679 CTCCTGCTCTCAGACCGGTCTTAAGCAAGGCGGTGGAATGACACACTCTCTCTTCTAGCG 2738
Db      782 TCCCTGCTCTTGAACCGGTCTTAAGCAAGGCGGTGGAATGACACACTCTCTCTTCTAAGC 841
QY      2739 GGT--GACTATAGAGAGAGTACCCCAAGCTGCTCAGAGAA 2782
Db      842 GGTAGACTTATAGAGAGTACCAAGGAATCGTTCAAGAGA 887

RESULT 10
LOCUS   AL543344                1201 bp    mRNA    linear    EST 31-MAY-2003
DEFINITION AL543344 Homo sapiens PLACENTA cot 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL543344
VERSION   AL543344.2 GI:31265191
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
L1, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12875822.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2864.r for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1001CF090P1cluster=2864.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0D1001CF090P1.

FEATURES
source      1..1201
              Location/Qualifiers
              1..1201
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0D1001YL17"
                /tissue="PLACENTA cot 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
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                sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT      277 a 373 c 315 g 214 t 22 others
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Query Match      25.3%; Score 783.4; DB 9; Length 1201;
Best Local Similarity 96.4%; Pred. No. 8.8e-196;
Matches 838; Conservative 5; Mismatches 21; Indels 5; Gaps 4;

QY      1714 TTTGGGACACTGATGGGATCCGATCCCTCTGCCCCAGACCAACCATCATGATTCG 1773
Db      221 TTTGGATGATGAAGCAAGGGATTCCTCCCTGCCCCAGACCAACCATCATGATTCG 280
QY      1774 ACGGCTCAAGAGGGGTATGAGTCTAGGGAGGAATCTGAGTGAAGCATCTGCTTGC 1833
Db      281 ACGGCTCAAGAGGGGTATGAGTCTAGGGAGGAATCTGAGTGAAGCATCTGCTTGC 340
QY      1834 TCACCTGACAGCAGACCCCTTTGGGGGACGTCTTCCCATATCCACAGACAAG 1893

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Db      341 TCACCTGACAGCAGACCCCTTTGGGGGAGAGTCTCTCCCATATATCCAAAGCAAGAG 400
QY      1894 GGAGTATTCGGGAAAGTACTCTCAAGAGCCACGACAGCTGGTCCCTGACCTCTTG 1953
Db      401 GGAGTATTCGGGAAAGTACTCTCAAGAGCCACGACAGCTGGTCCCTGACCTCTTG 460
QY      1954 GCCATTCAGTATCTGCTTCTGTCATGAGGGGCGCTTCTCGGGGATTCACGCTTC 2013
Db      461 GCCATTCAGTATCTGCTTCTGTCATGAGGGGCGCTTCTCGGGGATTCACGCTTC 520
QY      2014 TCCGCTGTGATCATGCGGCAAGACGTGGTGTGTGTGTCAGCGCAAGAGAGAGCTC 2073
Db      521 TCCGCTGTGATCATGCGGCAAGACGTGGTGTGTGTGTCAGCGCAAGAGAGAGCTC 580
QY      2074 ACCCACTGCGCGCGGCGCTCCATGAGCAGCGTCCACCAAGCTCAGCGGCTCTTGGGAGC 2133
Db      581 ACCCACTGCGCGCGGCGCTCCATGAGCAGCGTCCACCAAGCTCAGCGGCTCTTGGGAGC 640
QY      2134 ACTCAATCCAAAGACCCCAAGCGGAGGCGATCTCTGAGCGCCACTATGACAAAGGCAAG 2193
Db      641 ACTCAATCCAAAGACCCCAAGCGGAGGCGATCTCTGAGCGCCACTATGACAAAGGCAAG 699
QY      2194 CTGCGCACTCCCGGCAAGCAGCGCCAGATGCTATTAAAGCAGACAGACCACTGGAGC 2253
Db      700 CTGCGCACTCCCGGCAAGCAGCGCCAGATGCTATTAAAGCAGACAGACCACTGGAGC 759
QY      2254 CTGACGCGCCCTCCCGGCAAGCAGCGCCAGATGCTATTAAAGCAGACAGACCACTGGAGC 2313
Db      760 CTGACGCGCCCTCCCGGCAAGCAGCGCCAGATGCTATTAAAGCAGACAGACCACTGGAGC 819
QY      2314 CGCGGCAAGCGCGGAGTGGAGAGAGCAAGCAAGCTCATGATGCTGCAAAAGGACATG 2373
Db      820 CGCGGCAAGCGCGGAGTGGAGAGAGCAAGCAAGCTCATGATGCTGCAAAAGGACATG 879
QY      2374 CCCCCCATGGGCTCCCTGTGATTCACAGGAGCTGCCCCGCGGCTCCCGGAGCCAC 2433
Db      880 CCCCCCATGGGCTCCCTGTGATTCACAGGAGCTGCCCCGCGGCTCCCGGAGCCAC 939
QY      2434 ATCCCGAGCGGTGGTGTCTGCGCCATACAGAGAGGCTTACAGCATAGCTAGCTGAGC 2493
Db      940 ATCCCGAGCGGTGGTGTCTGCGCCATACAGAGAGGCTTACAGCATAGCTAGCTGAGC 999
QY      2494 CAGCCCAAAATGAGCGAGTGGGCCAGATGGCTGAGAGCAGCGCGGCAAGCTGGAG 2553
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QY      2554 TATTAAGCATCAAGAGACATCTCAGCAG 2582
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RESULT 11
LOCUS   B0678536                848 bp    mRNA    linear    EST 15-JUL-2002
DEFINITION B0678536 AGENCOURT_8208159 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262572
ACCESSION B0678536
VERSION   B0678536.1 GI:21791215
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
L1, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: DCTD/DM
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at:
<http://image.llnl.gov>
 Plate: LLCM2425 row: b column: 13
 High quality sequence stop: 695.

FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6262572"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_112"
 /note="Organ: Skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 210 a 207 c 231 g 199 t 1 others
 ORIGIN

Query Match 25.2%; Score 779.4; DB 13; Length 848;
 Best Local Similarity 98.1%; Pred. No. 8.1e-193;
 Matches 830; Conservative 0; Mismatches 12; Indels 4; Gaps 4;

QY 1286 CTGGGCCATATCAGCAATCAGCTGTTTCTGGATCAGAAAGGAATCTCTTGA 1345
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 Db 61 AGTTTGGCCAGAAATAGTGTGTTTCTAAATGACAGCTTTCTCGAGAGAGA 120
 QY 1406 TGAAGTGTTCACACTGGAATAATGACGATATGATGAGTCGAAAGCAATCATGG 1465
 Db 121 TGAAGTGTTCACACTGGAATAATGACGATATGATGAGTCGAAAGCAATCATGG 180
 QY 1466 GCATGACGCTGGACAGAGAGAGCTCTGTATGTTGGTCTCTACCTGTGTATA 1525
 Db 181 GCATGACGCTGGACAGAGAGAGCTCTGTATGTTGGTCTCTACCTGTGTATA 240
 QY 1526 AGGTTCCCTTGGCCGCTGTGAACGACATGGAGTAAATAAAACCTGTATTCCTCCA 1585
 Db 241 AGGTTCCCTTGGCCGCTGTGAACGACATGGAGTAAATAAAACCTGTATTCCTCCA 300
 QY 1586 GAGACCCATATTTGTGATGATTAAGAGAGGCTGCTCGACGCAATTTATCACCACAA 1645
 Db 301 GAGACCCATATTTGTGATGATTAAGAGAGGCTGCTCGACGCAATTTATCACCACAA 360
 QY 1646 GCAGACTGACTTTTGGACAGGACATAGACGCTGGCAATACAGATGCTGGGGAGTGC 1705
 Db 361 GCAGACTGACTTTTGGACAGGACATAGACGCTGGCAATACAGATGCTGGGGAGTGC 420
 QY 1706 ACAATTCCTTTGTGGCAGTCAATFGGGCAATTCAGTCCCTCTTGGCCACAGACACACAT 1765
 Db 421 ACAATTCCTTTGTGGCAGTCAATFGGGCAATTCAGTCCCTCTTGGCCACAGACACAT 480
 QY 1766 CAGATTGACGGGCTCAAGAGGGGTATGAGTCTAGGGGAGGATGCTGAGCTGGAAGCATC 1825
 Db 481 CAGATTGACGGGCTCAAGAGGGGTATGAGTCTAGGGGAGGATGCTGAGCTGGAAGCATC 540
 QY 1826 TGGTTGACTCAGCTACAGCAGACAGCCCTTTGGGGCAGTGTCTCCCATATACCCAG 1885
 Db 541 TGGTTGACTCAGCTACAGCAGACAGCCCTTTGGGGCAGTGTCTCCCATATACCCAG 600
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 Db 601 ACAAGAAGGAGTGTGGGAAAGTACTCTCAAGGCCAGCAGCAGAGCTGTGTTCCCGTCA 660

QY 1946 CCTCTTGGCCATATGACATCAGCTGCTGTCATGAGGGGCGCTTCTCGGGCATCA 2005
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 Db 721 CCGTCTACTGCGCTGTGTATCATCCGCGCAAGACCGTGTGTGTGTCAGCAGCAAGA 780
 QY 2064 GAAGGAGCTCACCACCT-CGCGCGGGGCTCCATGAG-CAGGCTACCAAGCTCAGCGG 2121
 Db 781 AAAGAGCTCACCACCTCAGCGCGGGGCTCCATGAGCAGGCTCAGCAAGCTCAGCGG 840
 QY 2122 CTCCTT 2127
 Db 841 CCTCT 846

RESULT 12
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 5', mRNA sequence.
 ACCESSION BUI72225
 VERSION BUI72225
 KEYWORDS EST.
 SOURCE BUI72225.1 GI:22686209
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC <http://mhc.nhl.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps@email.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Cloned by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLN at:
<http://image.llnl.gov>
 Plate: LLCM2347 row: m column: 16
 High quality sequence stop: 606.

FEATURES

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 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 215 a 229 c 238 g 201 t
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Query Match 25.0%; Score 772.4; DB 13; Length 883;
 Best Local Similarity 98.6%; Pred. No. 6e-193;
 Matches 779; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1301 ATCACAGTGTGTTTCTGGATCAGAAAGGAATCTTTGAAGTTTGGCCAGAA 1360
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QY      1601 GATGATTAAGAGAGTGTGTGCTGAGCCATTATACCCAAACAGACACTGACTTTG 1660
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QY      1661 AGCAGACATAGAGGTGGTGCATATACAGATGCTGTGGGAGCTGTACAAATTCCTTGTG 1720
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QY      1721 CACTGAATGGGATTCAGATTCCTCTTGCCAGCACAACCAATCATGATTCAGAGCTC 1780
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QY      1781 AAGAGGGTATGAGTCTGAGGAGAGATGCTGAGTGAAGCATCTGCTTACCTGCTG 1840
Db      494 AAGAGGGTATGAGTCTGAGGAGAGATGCTGAGTGAAGCATCTGCTTACCTGCTG 553
QY      1841 ACAGACACAGACCTTTGGGGGAGTGTCTCCATTAACCAAGACAGAGAGAGTGA 1900
Db      554 ACAGACACAGACCTTTGGGGGAGTGTCTCCATTAACCAAGACAGAGAGAGTGA 613
QY      1901 TTGCGGAAAGTTACTCTAAAGGCGACAGACAGTGTCCGTCACCTCTTGCGCATG 1960
Db      614 TTGCGGAAAGTTACTCTAAAGGCGACAGACAGTGTCCGTCACCTCTTGCGCATG 673
QY      1961 CAGTCATCTGGGCTTTGTGATAGGGGCGCTCTCTGTGGGATCAGCTTACGCTCT 2020
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QY      2081 CGGCGCGGGG 2090
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 VERSION B0440312.1 GI:21179388
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 864)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC/DCMP/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: L14M13504 row: c column: 07
 High quality sequence stop: 659.
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
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 Average insert size 2 kb. Library constructed by Life
 Technologies."

BASE COUNT 204 a 273 c 232 g 150 t 5 others

Query Match 24.9%; Score 770; DB 13; Length 864;
 Best Local Similarity 96.3%; Pred. No. 2.5e-192;
 Matches 830; Conservative 0; Mismatches 24; Indels 8; Gaps 4;

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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 652.
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 GGCAGCAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source
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 Location/Qualifiers

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 Best Local Similarity 99.2%; Pred. No. 1.2e-191;
 Matches 771; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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 SOURCE
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: DCTD/DRP
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LINC2425 row: c column: 04
 High quality sequence stop: 621.
 Location/Qualifiers

FEATURES

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:34:33 ; Search time 11072.7 Seconds

(without alignments)
11427.482 Million cell updates/sec

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Perfect score: 3093

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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9	2182.4	70.6	3041	6	BD159617 Homo sapi
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VERSION	AX026741.1	GI:10187886			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1				
AUTHORS	Klostermann, A. and Behl, C.				
TITLE	Human semaphorin 6a-1 (sema6a-1), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its				

JOURNAL

use as a potential drug target
 Patent: WO 0031252-A 1 02-JUN-2000;
 KLOSTERMANN ANDREAS (DE); MAX PLANCK GESELLSCHAFT (DE); BEHL
 CHRISTIAN (DE)

FEATURES

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RESULT 2

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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

KLSTERMANN, A. and Behl, C.

Human semaphorin 6a-1 (sema6a-1), a gene involved in neuronal development and regeneration mechanisms during apoptosis, and its use as a potential drug target

Journal

KLSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL CHRISTIAN (DE)

FEATURES

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 MEDLINE
 PUBMED
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QY	1681	AATACAGATGGCTGAGGGGACGTGTCACAAATTCCTTTGAGACATGATGGGCAATTCACAT	1740
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Db	841	GGCAACCTTTTCTACACCTTATPACAGCATCCCTGGGTCTGCAGTCTGTGCTATGACAT	900
QY	996	GCCTGACATGGCAGGTCTTTTACTGGGAGATTCAAGGAAACAGAACTTCCTGATTCCAC	1055
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QY	1056	CTGAGACACCGATTCTGTATGAACGAGTTCTTAAGCCACGACAGGTGTGTGTGGCTTC	1115
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RESULT 6
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to Mus musculus semaphorin 1A mRNA.
ACCESSION AK027867
VERSION AK027867.1 GI:14042853
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1
Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H.,
Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K.,
Arita,M., Nadekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J.,
Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuko,Y. and Oshima,A.,
NEDO human cDNA sequencing project
Unpublished
TITLE NEDO human cDNA sequencing project
JOURNAL
REFERENCE 2 (bases 1 to 6060)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
5'-& 3'-end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.
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ORIGIN
Query Match 96.0%; Score 2969.6; DB 9; Length 6060;
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Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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 VERSION AX099520.1 GI:13538594
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Jacobs,K., Mccoy,J.M., Lavallee,E.R., Collins-Racie,L.A., Evans,C.,
 Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.
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QY	121	TTTGGGGCCACAAAGCCAGAGACGGAACACACACAGAGGCACAGGCTGACATCCAGATG	180
Db	246	TTTGGGGCCACAAAGCCAGAGACGGAACACACACAGAGGCACAGGCTGACATCCAGATG	305
QY	181	ATTATGATCATGACGGAACCTCTACACTTGGCTAGGGACCAATTTATCTCTTTGAT	240
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QY	241	ATGAGACATTCACACGGAAGAAATTTATTTAGCAAAAACCTGCATGAAATTCAGA	300
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QY	841	TTGAACTGCTCAAGTTCTGAGAGCTCTCAITTTTATTTCAACATTTCTCCAGAGATTCAG	900
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Db	1026	GATGTATTCGTATCAACGGGCGGTATGTTGCTCCGGCAACGTTTCTACACTTAAAC	1085
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QY	1021	GGGAGATTCAAGGAACAGAAAGTCTCTGATTCACCTGACACCCAGTTCTGTATGAAGAGA	1080
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ACCESSION AF288666
VERSION AF288666.1 GI:11093908
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS
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Klostermann, A. and Behl, C.
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Db	1903	ATGGGGGGCCGTTCTCTGGGCAATCATGCTGATTTGTGGGATCACCGGCGCAAAAGC	1962
QY	2041	GTGGCTGTGTGACAGCGCAAGAGAGAGAGAGCTCACCCACTGGCGCGGGGGCTCCATGAGC	2100
Db	1963	GTGGCAGTATGTGGCGCAAGAGAGAGAGAGCTCACCTGCGTGGGGGATCTATGAGC	2022
QY	2101	AGGCTACCAAGCTATAGCGGCTCTTTGGGGGACCTCAATCCAAAGACCCAAAGCCGAG	2160
Db	2023	AGTGTCTCCGAGCTATAGTGGCTCTTTGGGGACCCAGCTCCAGTCCAAAGCCCTGAG	2082
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Db	2083	GGCATTCACAGCCACTCATGCAACAAGGCAAGCTGCGCACTCCGGGCAACGGGCTAAG	2142
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QY	2341	CAGAACTCATCAATCGTCGACAAAGAGACATGCCGCCATGGGCTCCCTGTGATTTCC	2400
Db	2263	CAGAACTCATCAATCGTCGACAAAGAGACATGCCGCCATGGGCTCCCTGTGATTTCC	2322
QY	2401	ACGAGACTGCCCCCTGGGGGCTCCCCAGCAGATCCCCAGCGGTGGGTCTCTCCCATC	2460
Db	2323	ACGAGACTGCCCCCTGGGGGCTCCCCAGCAGATCCCCAGCGGTGGGTCTCTCCCATC	2382
QY	2461	ACGAGAGAGGCTACCGAGATGAGTACGTGGACAGCCCAAAATGAGCGA--CGTGGC	2517

Db	2383	AGCCACGAGGCGTACCGACGACGATACGATACGATACGACCCAAATGAGCGAGTGGTGCT	2442		
QY	2518	CAGATGGCCCTGGAGGAGCACCAGGCCGCCACACTGGAGATATAGACCATATGAAAGACATCTCC	2577		
Db	2443	CAGATGGCACTGGAGAGCACCAGGCTGGCCACCTCGAGATATATGAACCCACCAAGAGACCTTG	2502		
QY	2578	AGCAGCAAGTGTCCCAACCATGGGGGTGAACCTTTGTGAGAACCTTGGAGACCTTGGACAGCTGGCCCCC	2637		
Db	2503	AGTATGATAGGTGCTCCCAACCATGGGGGTGAACCTTTGTGAGAACCTTGGAGACCTTGGACAGCTGGCCCCC	2562		
QY	2638	AAAGTTCCACAGCGGGAGAGGCTTCCCTGGGTGCCCCGGGGAGCTCCCTGTCTTACAGCCGT	2697		
Db	2563	AAAGTTCCACAGCGGGAGAGGCTTCCCTGGGTGCCCCGGGGAGCTCCCTGTCTTACAGCCGT	2622		
QY	2698	CTAAGCAAGCGGCTGGAAATAGCAACCACTGCTCTTCTTACGGGGTTGACTATTAAGAGAGC	2757		
Db	2623	CTGAGCAAGAGGCTGGAGATGACACATCTCTCTCTTATGGCTCGAATATTAAGAGAGC	2682		
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Db	2683	TACCCCAAGAACTGCTCCACAGAGAAAGCCACAGGCCACCACTCTCAAAAGAAACAACACT	2742		
QY	2818	AACCTCTCAATTCCTCTCAACCTCTCTCCAGAAACAGAGCTTTGGCGGGAGAGCAACCCG	2877		
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QY	2878	CCGCGCCGCCCGCAGAGAGGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATTTGGCCAG	2937		
Db	2803	CCGCGCCGCCCGCAGAGAGGGGTGACTCCATCCAGGTGCACAGCTCCAGCCATTTGGCCAG	2862		
QY	2938	GCCGTGACTGTCTGGAGGACAGCCCAAGGCTCTCAAGCCCTACAACTACAGACCAAGTGGGG	2997		
Db	2863	GCCGTGACTGTCTGGAGGACAGCCCAAGGCTCTCAAGCCCTACAACTACAGACCAAGTGGGG	2922		
QY	2998	CTGAAGCGACGCGCTCGCTAAAGCGGAGCTACCCGCCAAACCATCTTGTCTCCCTT	3057		
Db	2923	CTGAAGCGACGCGCTCGCTAAAGCGGAGCTACCCGCCAAACCATCTTGTCTCCCTT	2982		
QY	3058	TCCACATCCATGACAGCCCAATGATGCGTGTACATTA	3093		
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RESULT 9	BD159617	3041 bp	DNA	linear	PAT 17-JAN-2003
LOCUS	BD159617				
DEFINITION	Primer for synthesizing full-length cDNA and use thereof.				
ACCESSION	BD159617.1	GI:27865375			
VERSION	BD159617.1	GI:27865375			
KEYWORDS	JP 2002191363-A/14460.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 3041)				
AUTHORS	Ota,T., Isegai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Iishi,S., Sugiyaama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.				
TITLE	Primer for synthesizing full-length cDNA and use thereof				
JOURNAL	Patent: JP 2002191363-A/14460 09-JUL-2002;				
COMMENT	HELIIX RESEARCH INSTITUTE				
	OS Homo sapiens (human)				
	PN JP 2002191363-A/14460				
	PD 09-JUL-2002				
	PF 28-JUL-2000 JP 2000280990				
	PI TOSHIO OTA, TAKAO ISEGA, TERUSO NISHIKAWA, KOJI HAYASHI, KAORU				
	PI SAITO, YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,				
	PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,				
	PI KEIICHI NAGAI, TERUSO NISHIKAWA, KOJI HAYASHI, KAORU				
	PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/00, C12N15/02, C12N1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC				
	Primer for synthesizing full-length cDNA and use thereof FH				Key

FEATURES	FT	CDS	Location/Qualifiers
source			(85)..(2181).
Query Match	70.6%;	Score 2182.4;	DB 6; Length 3041;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2183;	Conservative	0; Mismatches	1; Indels 0; Gaps 0;
BASE COUNT	804 a	886 c	714 g 637 t
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QY	910	CGTATCAACGGGCGGATGTTGNCCTGGGAGAGGTTTCTACACCTTATAACACATCCCT	969
DB	1	CGTATCAACGGGCGGATGTTGNCCTGGGAGAGGTTTCTACACCTTATAACACATCCCT	60
QY	970	GGGCTGCAGTCTGTCCTATGACATGCTTGCATTTGCCAGTCTTTTATGGAGATTG	1029
DB	61	GGGCTGCAGTCTGTCCTATGACATGCTTGCATTTGCCAGTCTTTTATGGAGATTG	120
QY	1030	AAGGACACAAAGTCTCCTGATTCCACTGGACACCAAGTTCCTGATGAAAGAGATTCTTA	1089
DB	121	AAGGACACAAAGTCTCCTGATTCCACTGGACACCAAGTTCCTGATGAAAGAGATTCTTA	180
QY	1090	CCGAGCCAGAGTTGCTGTGCTGCTATCTCTTTAAGAATATGACCTCCATAGAG	1149
DB	181	CCGAGCCAGAGTTGCTGTGCTGCTATCTCTTTAAGAATATGACCTCCATAGAG	240
QY	1150	TTCCTCGATGATACCCCTGAACCTCATACAGACGCCGCCGCTCATGATGAGGACGTGCC	1209
DB	241	TTCCTCGATGATACCCCTGAACCTCATACAGACGCCGCCGCTCATGATGAGGACGTGCC	300
QY	1210	TTCATCTTCAACAGGCCATGGTTCCTGAGAACATGGTCAGATACCGCTTACCAAAATT	1269
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QY	1270	GCATGTGACACAGTGTGCGGCCCATATGATACATCACTGTGTGTTTCTGGGATCAGAG	1329
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QY	1330	AAGGAATCATCTTGAAGTTTGGCCAGAAATAGAAATAGTGGTTTCTAAATGACAGC	1389
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QY	1750	CCAGAGCAACACATCATGATTCAGAGGCTCAAGAGGGGTATGAGTTAAGGGAGGATG	1809
DB	841	CCAGAGCAACACATCATGATTCAGAGGCTCAAGAGGGGTATGAGTTAAGGGAGGATG	900

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RESULT 10
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AK027501 3041 bp mRNA linear PRI 01-AUG-2002
 Homo sapiens CDNA FLJ14595 fis, clone NT2RM002194, highly similar
 to Mus musculus semaphorin 7A mRNA.
 AK027501
 AK027501.1 GI:14042222
 Oligo capping: fis (full insert sequence).
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS
 1
 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
 Watanabe, M., Hosokawa, T., Kaku, Y., Kodaira, H., Kondo, H.,
 Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
 Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
 Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
 Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3041)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;
 Research Association for Biotechnology; cDNA library construction,
 5'- & 3'-end one pass sequencing and clone selection; Helix
 Research Institute (supported by Japan Key Technology Center etc.)
 and Department of Virology, Institute of Medical Science,
 University of Tokyo.

FEATURES
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BASE COUNT	804 a	886 c	714 g	637 t
ORIGIN				

Query Match	70.6%	Score 2182.4	DB 9	Length 3041
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2183	Conservative 0	Mismatches 1	Indels 0	Gaps 0

[illegible]

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QY	2530	GAGGACAGAGCGCGCACACTGGATATTAAGACATCAAGAAACATCTACGACGCAAGAT	2589
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QY	2590	CCCAACCATGGGGTGAACCTTGTGGAGAAACCTGGAGAGCGCTGCCCCCAAAGTTCACAG	2649
Db	1681	CCCAACCATGGGGTGAACCTTGTGGAGAAACCTGGAGAGCGCTGCCCCCAAAGTTCACAG	1740
QY	2650	CGGGAGGCTCTCCCTGGGTGCCCGCGGAGGCTCTCTGTCAGACCGGTTAAGCAAGCG	2709
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Db 2161 AAGCCCATGATGCGTGATACATA 2184

RESULT 11
AF030430 2770 bp mRNA linear ROD 15-NOV-1997
LOCUS Mus musculus semaphorin 1A mRNA, complete cds.
DEFINITION AF030430.1 GI:2623161
VERSION AF030430.1
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2770)
AUTHORS Zhou, L., White, F.A., Lentz, S.I., Wright, D.E., Fisher, D.A. and
Snider, W.D.
TITLE Cloning and expression of a novel murine semaphorin with structural
similarity to insect semaphorin 1
JOURNAL Mol. Cell. Neurosci. 9 (1), 26-41 (1997)
MEDLINE 97348468
PUBMED 9204478
REFERENCE 2 (bases 1 to 2770)
AUTHORS Zhou, L.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) Neurology, Washington University, 660 S.
Euclid Ave., St. Louis, MO 63110, USA

FEATURES
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 Oca, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
 Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 Primer for synthesizing full-length cDNA and use thereof
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LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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 Iisogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
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Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuko, Y., Ninomiya, K., and Iwayanagi, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2293)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan: cDNA full insert construction; Research Association for Biotechnology; cDNA library construction; 5'-3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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FEATURES

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LOCUS BD127394 2227 bp DNA linear PAT 18-SEP-2002

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD127394

VERSION BD127394.1 GI:23222339

KEYWORDS JP 2002017375-A/2825.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2227)

AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002017375-A 2825 22-JAN-2002;

HEALTH RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017375-A/2825

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253172

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PI YUKI KAWAI, AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI SHINICHI KOJIMA,

PI TETSUJI OTSUKI,HISASHI KOGA

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Matches 1743; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1741 ATAA 1744

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LOCUS AK074975 Homo sapiens CDNA FLJ90494 fls, clone NT2RP3003614.

ACCESSION AK074975

VERSION AK074975.1 GI:22760768

KEYWORDS oligo capping; fls (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T., Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S., Kawai-Hio, Y., Saito, K., Yamamoto, J., Makamatsu, A., Nakamura, Y., Kojima, S., Nagahara, K., Masudo, Y., Ono, T., Okano, K., Yoshikawa, Y., Aotsuka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and Niimura, K.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2227)

AUTHORS Isogai, T. and Otsuki, T.

TITLE Direct Submission

JOURNAL Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction: Institute of Medical Science, University of Tokyo; Laboratory of Genome Structure, Human Genome Center; cDNA 5'-3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).

FEATURES

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BASE COUNT 567 a 700 c 560 g 400 t

ORIGIN

Query Match 56.3%; Score 1742.4; DB 9; Length 2227;

Best local similarity 99.9%; Pred. No. 0;

Matches 1743; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1350 TTGGCCAGAAATGGAATAGTGTTTCTTAATGACAGCTTTCTGGAGAGATGAG 1409

Db 1 1TTGGCCAGAAATGGAATAGTGTTTCTTAATGACAGCTTTCTGGAGAGATGAG 60

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Db 61 TGTTCACACTCGAAATAATGACGATATGATGAGAGTGAAGCAAAAGATCATGGGCAT 120

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 PT therapeutic agent, for modulating immune system, in gene therapy or for
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 PS Claim 1; Fig 2; 53pp; English.
 XX The present sequence is a cDNA encoding transmembranous human semaphorin
 CC 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal development and
 CC regeneration mechanisms during apoptosis. Semaphorin is a family of
 CC proteins displaying secreted or transmembrane-based repulsive guidance
 CC cues critically involved in neuronal development. The present sequence
 CC was isolated from human 1-ZAP Express cDNA library which was screened
 CC using a PCR fragment amplified from human neuroblastoma cell line
 CC SK-N-MC cDNA. The (HSA)SEMA6A-1 protein contains a zyxin-like domain
 CC that selectively binds to members of Eln/VASP protein family especially
 CC Eln. Expression of (HSA)SEMA6A-1 is highest in embryonic brain and
 CC kidney and moderate in lung. The present sequence is useful as diagnostic
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 CC and plasticity.
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 DB 2098 GAGTGGAGAGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2157
 QY 1501 GTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 DB 2158 GTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2217
 QY 1561 TGTAAATAAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620

Db 2218 TGTAAAAAACCTGATATGCTCCAGAGACCATATGTGATGATTAAGAAAGTGTG 2277
 QY 1621 GGCTGAGCATTTATACCCCAACAGAGACTGATTTGACAGAGACTAAGAGGTGAC 1680
 Db 2278 GCTTCAGCATTTATACCCCAACAGAGACTGATTTGACAGAGACTAAGAGGTGAC 2337
 QY 1681 AATAGAGATGATCTGGGGAGTGTCAATTCCTTTGTGGCACTGAATGGGATTCAGT 1740
 Db 2338 AATAGAGATGATCTGGGGAGTGTCAATTCCTTTGTGGCACTGAATGGGATTCAGT 2397
 QY 1741 TCCCTCTTGGCCAGACAAACATCAGATTGAGGGCTCAAGAGGGGTATGATCTAG 1800
 Db 2398 TCCCTCTTGGCCAGACAAACATCAGATTGAGGGCTCAAGAGGGGTATGATCTAG 2457
 QY 1801 GGAGAGATGCTGAGCGAAGATGCTGCTTGAACCTGACAGACAGACCTTTGGGG 1860
 Db 2458 GGAGAGATGCTGAGCGAAGATGCTGCTTGAACCTGACAGACAGACCTTTGGGG 2517
 QY 1861 GAGATGCTTCCCATATCACCAGACAAAGAGAGATTCGGGAAAGTTACTCTAA 1920
 Db 2518 GAGATGCTTCCCATATCACCAGACAAAGAGAGATTCGGGAAAGTTACTCTAA 2577
 QY 1921 GGCCAGAGCAAGCTGCTCCGCTACCCCTCTTGGCCATTGACATCTCTGCTTTCGTC 1980
 Db 2578 GGCCAGAGCAAGCTGCTCCGCTACCCCTCTTGGCCATTGACATCTCTGCTTTCGTC 2637
 QY 1981 ATGGGGCCGCTCTTCGCGGACATCAGCTCTGCTGCTGATGATGGGCAAGAG 2040
 Db 2638 ATGGGGCCGCTCTTCGCGGACATCAGCTCTGCTGCTGATGATGGGCAAGAG 2697
 QY 2041 GTGGCTGTGTGAGCGCAAGAGAGAGAGCTACCCACTGCGCGCGGGGCTCCATGAGC 2100
 Db 2698 GTGGCTGTGTGAGCGCAAGAGAGAGAGCTACCCACTGCGCGCGGGGCTCCATGAGC 2757
 QY 2101 AGCGTACCAAGCTCAGCGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160
 Db 2758 AGCGTACCAAGCTCAGCGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2817
 QY 2161 GCCATGCTACGGCACTCAGTACGACAAAGGCAAGCTGCGCACTCCGCGCAACAGCGCAAG 2220
 Db 2818 GCCATGCTACGGCACTCAGTACGACAAAGGCAAGCTGCGCACTCCGCGCAACAGCGCAAG 2877
 QY 2221 ATGCTCATTAAGCAGACAGCAACCACTTGACCTGACGGCCCTCCCAACCCCAAGATCA 2280
 Db 2878 ATGCTCATTAAGCAGACAGCAACCACTTGACCTGACGGCCCTCCCAACCCCAAGATCA 2937
 QY 2281 ACCCAACGCTGACAG 2340
 Db 2938 ACCCAACGCTGACAG 2997
 QY 2341 CAGACCTCATCAATGCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
 Db 2998 CAGACCTCATCAATGCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3057
 QY 2401 ACGGACCTGCTCCCTGCGGGGCTCCCGAGCCACATCCCAAGCTGCTGCTGCTCCCATC 2460
 Db 3058 ACGGACCTGCTCCCTGCGGGGCTCCCGAGCCACATCCCAAGCTGCTGCTGCTCCCATC 3117
 QY 2461 ACGGACCTGCTCCCTGCGGGGCTCCCGAGCCACATCCCAAGCTGCTGCTGCTCCCATC 2520
 Db 3118 ACGGACCTGCTCCCTGCGGGGCTCCCGAGCCACATCCCAAGCTGCTGCTGCTCCCATC 3177
 QY 2521 ATGGGCTGAG 2580
 Db 3178 ATGGGCTGAG 3237
 QY 2581 AGCAAGAGTCCCAACCATGAGGATGAACTTGTGAGAACTGGAACGCTGCCGCCCAAA 2640
 Db 3238 AGCAAGAGTCCCAACCATGAGGATGAACTTGTGAGAACTGGAACGCTGCCGCCCAAA 3297
 QY 2641 GTTCACAGAGGGAG 2700

Db 3298 GTTCCACAGCGGGAGAGCTCCCTGGGTCCCGGGAGAGCTCCCTGTCTCAGACCGGTCTA 3357
 QY 2701 AGCAAGCGGCTGGAATATGACCACTCTCTCTTCTACGGGGTGTGACTATTAAGAGAGCTAC 2760
 Db 3358 AGCAAGCGGCTGGAATATGACCACTCTCTCTTCTACGGGGTGTGACTATTAAGAGAGCTAC 3417
 QY 2761 CCCAGAGTCTGCTCAG 2820
 Db 3418 CCCAGAGTCTGCTCAG 3477
 QY 2821 TCTCCATATCTCTCAGCTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880
 Db 3478 TCTCCATATCTCTCAGCTCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3537
 QY 2881 CCCGCCCCAG 2940
 Db 3538 CCCGCCCCAG 3597
 QY 2941 GTGACTGTCTCGAGGAG 3000
 Db 3598 GTGACTGTCTCGAGGAG 3657
 QY 3001 AAGCGTACGCGCT 3060
 Db 3658 AAGCGTACGCGCT 3717
 QY 3061 ACATCCATGAAGCCCAATGATGCTGTACATAA 3093
 Db 3718 ACATCCATGAAGCCCAATGATGCTGTACATAA 3750
 Db 3718 ACATCCATGAAGCCCAATGATGCTGTACATAA 3750
 RESULT 2
 ID AAA93617 standard; DNA; 3498 BP.
 AC AAA93617;
 AC 16-JAN-2001 (first entry)
 DT
 XX
 DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
 XX
 KW SFXC protein; human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour;
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; stenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cytoskeletal; immunosuppressive;
 KW anti-HIV; anti-inflammatory; antiarthritic; antiarteriosclerotic;
 KW neuroprotective; vulnerability; anti-allergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.
 OS Homo sapiens.
 XX
 PN W0200053742-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000MO-US06280.
 XX
 PR 09-MAR-1999; 99US-0123667.
 PR 08-MAR-2000; 2000US-0123667.
 XX
 PA (CURA-) CURAGEN CORP.
 PA
 PI Shinkets RA;
 XX
 DR WPI: 2000-594318/56.
 DR P-PSDB: AAB23030.
 XX
 PT Novel human membrane associated or secreted polypeptides and
 PT polynucleotides useful for diagnosis, prevention and treatment of
 PT pathological states such as cancer, immune, cardiovascular and

PT neurological disorders -
 XX
 PS Claim 3; Fig 2; 151pp; English.

CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
 CC which encode human SECX proteins (AA933029-B23048). The SECX proteins
 CC and act as regulator of cellular proliferation and differentiation. SECX
 CC proteins or nucleotides are useful for diagnosing the presence of, or
 CC predisposition to, a disease associated with altered levels of SECX
 CC proteins and nucleotides. The SECX proteins are also useful to screen
 CC compounds that modulate SECX activity or expression. The interaction of
 CC a SECX protein with other cellular proteins may be useful to modulate
 CC the activity of a partner protein, cellular proliferation, cellular
 CC differentiation and cell survival. SECX nucleotides are useful for the
 CC recombinant expression of SECX protein, and may be used to detect SECX mRNA
 CC or genetic lesions in the SECX gene. They may also be used to modulate
 CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
 CC acid sequences are also useful for identifying a cell or tissue type in
 CC a biological sample, and in forensic biology. SECX primers or probes are
 CC useful for detecting the presence of SECX nucleotides and for screening
 CC tissue cultures for contamination. Diseases that may be treated or
 CC prevented using SECX proteins or nucleotides include cancer (e.g.,
 CC colorectal carcinoma, prostate cancer), benign tumors, immune disorders
 CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
 CC infections, inflammatory disorders, arthritis, hematopoietic disorders,
 CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
 CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
 CC surgical or traumatic wounds, spinal cord injury), and skeletal
 CC disorders.

XX
 CC Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 1 other;

Query Match 98.2%; Score 3038; DB 21; Length 3498;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 3072; Conservative 0; Mismatches 21; Indels 2; Gaps 2;

QY 1 ATGAGTCAAGACCTTCTGCTATATTTACACATGCTACACTTTGCTGGGCTGTTTC 60
 DB 214 ATGAGTCAAGACCTTCTGCTATATTTACACATGCTACACTTTGCTGGGCTGTTTC 273
 QY 61 CCAGAAAGATTGAGCCATTCGATTTTGGCATGGCACTATACAAAAGATCCGGTG 120
 DB 274 CCAGAAAGATTGAGCCATTCGATTTTGGCATGGCACTATACAAAAGATCCGGTG 333
 QY 121 TTGTGGCCACAAGCCAGGAGGAAACACACACAGAGGACAGGCTGACATCCAGATG 180
 DB 334 TTGTGGCCACAAGCCAGGAGGAAACACACACAGAGGACAGGCTGACATCCAGATG 393
 QY 181 ATTATGATCATGAAGGAAACCTCTACATTTGCTAGGACCATTTATACCTGTGAT 240
 DB 394 ATTATGATCATGAAGGAAACCTCTACATTTGCTAGGACCATTTATACCTGTGAT 453
 QY 241 ATAGACATCAACACGGAAGAAATTTATGTAGCAAAAACCTGATGGAATTTAA 300
 DB 454 ATAGACATCAACACGGAAGAAATTTATGTAGCAAAAACCTGATGGAATTTAA 513
 QY 301 CAGGCCGATGTAGACATGCAAGATGAAGGAAAAATTAAGATAGTGCACAACTTT 360
 DB 514 CAGGCCGATGTAGACATGCAAGATGAAGGAAAAATTAAGATAGTGCACAACTTT 573
 QY 361 ATTAAGTCTTCTAAAGAAAAACGATGATGCTTTTGTCTGTGGAACATATGCTTC 420
 DB 574 ATTAAGTCTTCTAAAGAAAAACGATGATGCTTTTGTCTGTGGAACATATGCTTC 633
 QY 421 AACCCCTTCTGCAAGAACTATAAGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 634 AACCCCTTCTGCAAGAACTATAAGATGATGATGATGATGATGATGATGATGATGAT 693
 QY 481 GGAATGGCAGATGCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 694 GGAATGGCAGATGCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 753

QY 541 AAACATACCTAGCCACAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 754 AAACATACCTAGCCACAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 813
 QY 601 CTTGGAGAAAGCCCTTACCTCGGACCCGTCAGACAGATTCAAATATGTTGAAAGACA 660
 DB 814 CTTGGAGAAAGCCCTTACCTCGGACCCGTCAGACAGATTCAAATATGTTGAAAGACA 873
 QY 661 TACTTTGTTCAAGCCGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 874 TACTTTGTTCAAGCCGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 933
 QY 721 GTGGATATTAACCATGGAAGAGTATGTTTCCCAAGAGTGGCTCAGTTGTAAGAT 780
 DB 934 GTGGATATTAACCATGGAAGAGTATGTTTCCCAAGAGTGGCTCAGTTGTAAGAT 993
 QY 781 GATATGGAGGATTCATCAAGAGTCTCTGAGGAAACAGTGAACGCTGCTGAAGGGGCG 840
 DB 994 GATATGGAGGATTCATCAAGAGTCTCTGAGGAAACAGTGAACGCTGCTGAAGGGGCG 1053
 QY 841 TTGAAGTGTCAAGTCTGAGACATCTCATTTTATTTTCAACATTCCTCCAGCAGTTACA 900
 DB 1054 TTGAAGTGTCAAGTCTGAGACATCTCATTTTATTTTCAACATTCCTCCAGCAGTTACA 1113
 QY 901 GATGATTCATCAACAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 1114 GATGATTCATCAACAGGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 1173
 QY 961 AGCATCCCTGGGCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 DB 1174 AGCATCCCTGGGCTGAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1233
 QY 1021 GGGAGATTCAGAGACAGAGTCTCTGATTCACACCTGAGACACACCTCTGATGAGCA 1080
 DB 1234 GGGAGATTCAGAGACAGAGTCTCTGATTCACACCTGAGACACACCTCTGATGAGCA 1293
 QY 1081 GTTCTTAACCCAGGCGAGT 1140
 DB 1294 GTTCTTAACCCAGGCGAGT 1353
 QY 1141 TCCAAATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1354 TCCAAATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1413
 QY 1201 GCAATGCCCTCATCTTCAACAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
 DB 1414 GCAATGCCCTCATCTTCAACAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1473
 QY 1261 ACCAAATTTGAGTGGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
 DB 1474 ACCAAATTTGAGTGGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1533
 QY 1321 GGATCAGAGAGGAAATCATCTTGAAGTTTGTGGCCAGATTAAGAAATATGTTTCTTA 1380
 DB 1534 GGATCAGAGAGGAAATCATCTTGAAGTTTGTGGCCAGATTAAGAAATATGTTTCTTA 1593
 QY 1381 AATGACAGCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 DB 1594 AATGACAGCTTTTCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1653
 QY 1441 GGAATGAGAGCAAAAGAGATCATGAGGATGATGATGATGATGATGATGATGATGATGAT 1500
 DB 1654 GGAATGAGAGCAAAAGAGATCATGAGGATGATGATGATGATGATGATGATGATGATGAT 1713
 QY 1501 GTTGGCTTCTAAGCTGT 1560
 DB 1714 GTTGGCTTCTAAGCTGT 1773
 QY 1561 TGTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 DB 1774 TGTAAAGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833
 QY 1621 GCTTCAGGCAATTTATCAACCAACAGCAGATGATGATGATGATGATGATGATGATGAT 1680

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Db      1834  GCGTCAGACATTATACACCACACAGCAGCTGACTTTGAGAGGACATAGAGCGGTGC 1893
QY      1681  AATACAGATGCTGGGGGAGCTGTCAATATCTTTGTGGCACTGATGAGGCTTCAGT 1740
Db      1894  AATACAGATGCTGGGGGAGCTGTCAATATCTTTGTGGCACTGATGAGGCTTCAGT 1953
QY      1741  TCCCTCTGCCAGCAGCAACACATCAGATTGACGGCTCAGAGGGGATATGAGTACG 1800
Db      1954  TCCCTCTGCCAGCAGCAACACATCAGATTGACGGCTCAGAGGGGATATGAGTACG 2013
QY      1801  GAGGAGATGCTGAGACTGGAAGCATCTGCTTGAATCTGACAGCAGACAGCCCTTGG 1860
Db      2014  GAGGAGATGCTGAGACTGGAAGCATCTGCTTGAATCTGACAGCAGACAGCCCTTGG 2073
QY      1861  GCAGTCTTCCATATATCCAAAGAGAGAGAGGATGATGGGAAATGTTACTTCAAA 1920
Db      2074  GCAGTCTTCCATATATCCAAAGAGAGAGAGGATGATGGGAAATGTTACTTCAAA 2133
QY      1921  GAGCAGAGACAGCTGCTTCCGCTACCCCTCTTGGCCATGTCAGTCACTCTTCTGTC 1980
Db      2134  GAGCAGAGACAGCTGCTTCCGCTACCCCTCTTGGCCATGTCAGTCACTCTTCTGTC 2193
QY      1981  ATGGGGGCGCTCTTCTTGGGAGCATACCCCTGCTGCTGTATCATGCGGGGAGAAAG 2040
Db      2194  ATGGGGGCGCTCTTCTTGGGAGCATACCCCTGCTGCTGTATCATGCGGGGAGAAAG 2253
QY      2041  GTGGCTGTGTGAGCGCAAGAGAGAGAGAGCTACCCACTGCGCGCGGCTCCATGAGC 2100
Db      2254  GTGGCTGTGTGAGCGCAAGAGAGAGAGAGCTACCCACTGCGCGCGGCTCCATGAGC 2313
QY      2101  AGCGTCACCAAGCTCAGCGGCTCTTCTTGGGAGCATCAATCCAAAGACCCAAAGCC 2160
Db      2314  AGCGTCACCAAGCTCAGCGGCTCTTCTTGGGAGCATCAATCCAAAGACCCAAAGCC 2373
QY      2161  GCCATCTCTCAAGCCATCATGCAACAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db      2374  GCCATCTCTCAAGCCATCATGCAACAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2433
QY      2221  ATGTCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2280
Db      2434  ATGTCTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2493
QY      2281  ACCCCAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db      2494  ACCCCAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2553
QY      2341  CAGAACTCTCATCATGCTCTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400
Db      2554  CAGAACTCTCATCATGCTCTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2613
QY      2401  ACAGAGCTGCGCCCTGCGGGGCTTCCCGCAGCAGCATCCAGCTGTTGTTCTCCATC 2460
Db      2614  ACAGAGCTGCGCCCTGCGGGGCTTCCCGCAGCAGCATCCAGCTGTTGTTCTCCATC 2673
QY      2461  ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db      2674  ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2733
QY      2521  ATGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db      2734  ATGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2793
QY      2581  AGCAAGAGTCCCAACCATGAGGAGTGAACCTTGTGAGAGAGAGAGAGAGAGAGAG 2640
Db      2794  AGCAAGAGTCCCAACCATGAGGAGTGAACCTTGTGAGAGAGAGAGAGAGAGAGAG 2853
QY      2641  GTTCCACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
Db      2854  GTTCCACAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2913
QY      2701  AGCAAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760

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Db      2914  AGCAAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2973
QY      2761  CCCAGAGACTGCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2819
Db      2974  CCCAGAGACTGCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3033
QY      2820  CTCCTCCATCTCTCTTC - ACCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2878
Db      3034  CCCAGAGACTGCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3093
QY      2879  CGCCCGCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2938
Db      3094  CGCCCGCCCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3153
QY      2939  CGGTGACTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2998
Db      3154  CGGTGACTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3213
QY      2999  TGAAGGCTAGCGCCCTGCTAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3058
Db      3214  TGAAGGCTAGCGCCCTGCTAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3273
QY      3059  CCACATCCATGAAGCCCATGATGCGGTACATGA 3093
Db      3274  CCACATCCATGAAGCCCATGATGCGGTACATGA 3308

RESULT 3
ID  ABX71103 standard; cDNA; 4280 BP.
AC  ABX71103;
DE  05-MAR-2003 (first entry)
XX
XX  Novel human cDNA sequence #328.
DE
XX  Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW  Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW  neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW  autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW  insulin-dependent diabetes mellitus; anaemia; thrombocytopenia; wound;
KW  ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW  fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW  coagulation disorder; cancer; tumour; inflammatory disease;
KW  septic shock; Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW  differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW  haemostatic; antiinflammatory; expressed sequence tag; EST.
OS  Homo sapiens.
XX
XX  WO200281731-A2.
XX
XX  17-OCT-2002.
XX
XX  29-JAN-2002; 2002WO-US01222.
XX
XX  30-JAN-2001; 2001US-0774528.
XX
XX  (HYSE-) HYSEQ INC.
XX  (GOOD) GOODRICH R W.
XX
XX  Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX  Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Dmanac RT;
XX
XX  WPI; 2003-058563/05.
XX
XX  Novel polypeptide useful for treating neurodegenerative diseases,
XX  myeloid or lymphoid cell disorders, bone disorders, mechanical and
XX  traumatic disorders, coagulation disorders, and inflammatory diseases
XX
XX  Claim 1; Page -; 612pp; English.

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xx This invention relates to the cDNA sequences encoding an isolated novel human polypeptide. The protein encoded by the nucleic acid of the invention is useful for treating central and peripheral nervous system diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease, Alzheimer's disease); autoimmune disease (e.g. systemic lupus erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus); myeloid or lymphoid cell disorders (e.g. anemia and thrombocytopenia); wounds, ulcers, burns, bone disorders (e.g. osteoporosis, osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head trauma); lung or liver fibrosis; reperfusion injury in various tissues; bacterial, viral or fungal infections; allergic conditions such as allergic rhinitis, asthma; coagulation disorders (e.g. hemophilia); cancer and tumors; and inflammatory diseases (e.g. septic shock, Crohn's disease, anaphylaxis). The protein may be used to inhibit the growth, infection or function of infectious agents such as bacteria, fungi, viruses, or to effect bodily characteristics, CC biohythms or circadian cycles of rhythms. The protein may also have proliferation/differentiation, stem cell growth factor, haematopoiesis regulation, immune stimulating or suppressing, chemotactic/chemokinetic, hemostatic and thrombolytic receptor/ligand, and antiinflammatory activities. The cDNA sequences of the invention are useful for expressing recombinant protein for analysis. The present CC sequence represents a novel human cDNA sequence of the invention, CC this sequence is an expressed sequence tag (EST) and was identified CC using subtractive hybridisation.

xx Sequence 4280 BP; 1185 A; 1165 C; 1001 G; 929 T; 0 other;

Query Match 98.0%; Score 3032; DB 25; Length 4280;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 3093; Conservative 0; Mismatches 0; Indels 51; Gaps 1;

QY 1 ATGAGGTGAGAACGCTTGTCTGCTATTTTTCACACTGCTACACTTCTGGGCTGGTTTC 60
 DB 267 ATGAGGTGAGAACGCTTGTCTGCTATTTTTCACACTGCTACACTTCTGGGCTGGTTTC 326
 QY 61 CCGAAGATTTGAGCAATGAGTATTTGCGATGGAACATATACAAACAGTATCCGCTG 120
 DB 327 CCGAAGATTTGAGCAATGAGTATTTGCGATGGAACATATACAAACAGTATCCGCTG 386
 QY 121 TTGTGGGCCAAGCCAGGAGCAACACACACAGAGCCAGCTGGCATCCAGATG 180
 DB 387 TTGTGGGCCAAGCCAGGAGCAACACACACAGAGCCAGCTGGCATCCAGATG 446
 QY 181 ATTATGATCATGAGGAACCCCTCATTTGCTGAGGACCATATTTTACTGTTGAT 240
 DB 447 ATTATGATCATGAGGAACCCCTCATTTGCTGAGGACCATATTTTACTGTTGAT 506
 QY 241 ATGAGCATCACACAGAGAAATTTATGTAGCAAAAACGTGACATGGAATCTAGA 300
 DB 507 ATGAGCATCACACAGAGAAATTTATGTAGCAAAAACGTGACATGGAATCTAGA 566
 QY 301 CAGGCCGATGACACATCGAGATGAGGAAACATTAAGTATGATGCCACACTTT 360
 DB 567 CAGGCCGATGACACATCGAGATGAGGAAACATTAAGTATGATGCCACACTTT 626
 QY 361 ATTAAAGTCTTTAAAGAAAAAGATGATGATTTGTTGCTGTGAACTAATGCCCTTC 420
 DB 627 ATTAAAGTCTTTAAAGAAAAAGATGATGATTTGTTGCTGTGAACTAATGCCCTTC 686
 QY 421 AACCCCTGTCAGAAACTATAGATGATGATGGAACCATTCGGGGATGATTTAGC 480
 DB 687 AACCCCTGTCAGAAACTATAGATGATGATGGAACCATTCGGGGATGATTTAGC 746
 QY 481 GGAATGGCCAGATGCCCATATGATGCCAATGCCAAGCTTGATGCTTTGCAAGTGA 540
 DB 747 GGAATGGCCAGATGCCCATATGATGCCAATGCCAAGCTTGATGCTTTGCAAGTGA 806
 QY 541 AAACATATCTAGCCACAGTACTGATCTTCTGCAATGACGAGCATTTACCGAGGT 600
 DB 807 AAACATATCTAGCCACAGTACTGATCTTCTGCAATGACGAGCATTTACCGAGGT 866

QY 601 CTGAGAGAAAGCCCTACCTCGGAGCCGTCAAGACGATTCATAAATGTTGAAAGACCA 660
 DB 867 CTTGAGAGAAAGCCCTACCTCGGAGCCGTCAAGACGATTCATAAATGTTGAAAGACCA 926
 QY 661 TACTTGTTCAGCCGCTGATTTACGAGATTTATCTACTTCTTTCAGGAAATATACA 720
 DB 927 TACTTGTTCAGCCGCTGATTTACGAGATTTATCTACTTCTTTCAGGAAATATACA 986
 QY 721 GTGGAGTATTAACCATGGAGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGAAGAT 780
 DB 987 GTGGAGTATTAACCATGGAGAAAGTAGTTTCCCAAGAGTGGCTCAGGTTTGAAGAT 1046
 QY 781 GATATGGAGATTCCTCAAGAGTCTCGAAGAAACAGTGAAGCTGTTCTTGAAGCGCC 840
 DB 1047 GATATGGAGATTCCTCAAGAGTCTCGAAGAAACAGTGAAGCTGTTCTTGAAGCGCC 1106
 QY 841 TTGAACCTGCTAGTTCTGAGACCTCTCATTTTATTTTCAATCTCCAGGAGTTTACA 900
 DB 1107 TTGAACCTGCTAGTTCTGAGACCTCTCATTTTATTTTCAATCTCCAGGAGTTTACA 1166
 QY 901 GATGATTCGTATCAACAGGCGGTGATGTTGCTCGCAACGTTTCTACACCTTATAC 960
 DB 1167 GATGATTCGTATCAACAGGCGGTGATGTTGCTCGCAACGTTTCTACACCTTATAC 1226
 QY 961 AGCATCCCTGGGCTGCTGCACTGCTGCTATGACATCTTGACATTCGCCAGTGTCTTACT 1020
 DB 1227 AGCATCCCTGGGCTGCTGCACTGCTGCTATGACATCTTGACATTCGCCAGTGTCTTACT 1286
 QY 1021 GGGAGATTCAGAGAAAGAAAGTCTCTGATTCACCTGAGACACCATTCCTGATGAACGA 1080
 DB 1287 GGGAGATTCAGAGAAAGAAAGTCTCTGATTCACCTGAGACACCATTCCTGATGAACGA 1346
 QY 1081 GTTCTTAAGCCCGAGGCGAGTGTGCTGCTGCTCATCTCTTAAGAAATATGCAAC 1140
 DB 1347 GTTCTTAAGCCCGAGGCGAGTGTGCTGCTGCTCATCTCTTAAGAAATATGCAAC 1406
 QY 1141 TCCATAGATTTCCCTGATGATACCTTGAACTTATCAAGAGCAACCGCTCATGAGATGAG 1200
 DB 1407 TCCATAGATTTCCCTGATGATACCTTGAACTTATCAAGAGCAACCGCTCATGAGATGAG 1466
 QY 1201 GCAGTGGCCCTCATCTCTCAACAGGCGATGTTGCTGAGAAATGTCAGATACCGGCTT 1260
 DB 1467 GCAGTGGCCCTCATCTCTCAACAGGCGATGTTGCTGAGAAATGTCAGATACCGGCTT 1526
 QY 1261 ACCAAATTTGCACTGACACAGCTGCTGGCCATATCAGATCAGATGCTGTTTCTG 1320
 DB 1527 ACCAAATTTGCACTGACACAGCTGCTGGCCATATCAGATCAGATGCTGTTTCTG 1386
 QY 1321 GATCAGAGAAAGGAATCATCTGGAATTTTGGCCAGAAATAGGAATAGTGTCTTCTA 1380
 DB 1587 GATCAGAGAAAGGAATCATCTGGAATTTTGGCCAGAAATAGGAATAGTGTCTTCTA 1646
 QY 1381 AATGACAGCTTTTCTGAGAGATAGTGTTTTACAACCTCTGAAAAATGACGATATGAT 1440
 DB 1647 AATGACAGCTTTTCTGAGAGATAGTGTTTTACAACCTCTGAAAAATGACGATATGAT 1706
 QY 1441 GGAATGAGCAAAAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 DB 1707 GGAATGAGCAAAAGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1766
 QY 1501 GTTCCGTTCTTACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 DB 1767 GTTCCGTTCTTACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1826
 QY 1561 TGTAAAAAAACCTTATGCTTCCAGAGAACCATATGATGATGATGATGATGATGATGAT 1620
 DB 1827 TGTAAAAAAACCTTATGCTTCCAGAGAACCATATGATGATGATGATGATGATGATGAT 1886
 QY 1621 GCGTGCAGCAATTTATACCCCAAGACAGACTGTTTGAAGAGATATGAGAGGTC 1680
 DB 1887 GCGTGCAGCAATTTATACCCCAAGACAGACTGTTTGAAGAGATATGAGAGGTC 1946

QY 1681 AATACAGATGTCGTGGGGGACTGTCAATTCCTTTGTGGCACTGA----- 1726
 1947 AATACAGATGTCGTGGGGGACTGTCAAAATTCCTTTGTGGCACTGAATGATTCACATTCACATTC 2006
 QY 1727 -----ATGGGCAATTCACATTCCTTTGTGG 1749
 2007 CCTCTACAGATGATGAAATGTCCTTACAAACAGATGATGGGCAATTCACATTCCTTTGTGG 2066
 QY 1750 CCAGAGCAACCAATCAGATTCAGAGGGCTCAGAGGGGATGAGTCTAGGGGAGGATG 1809
 2067 CCAGAGCAACCAATCAGATTCAGAGGGCTCAGAGGGGATGAGTCTAGGGGAGGATG 2126
 QY 1810 CTGAGCTGAGAGCATCTGCTTGAATCACTGACAGCAGACAGCCCTTTGGGGGAGTCT 1869
 2127 CTGAGCTGAGAGCATCTGCTTGAATCACTGACAGCAGACAGCCCTTTGGGGGAGTCT 2186
 QY 1870 TCCCATATATACCAAGACAAGAGGAGTATTCGGGAAAGTTACTCTAAAGCCACAGAC 1929
 2187 TCCCATATATACCAAGACAAGAGGAGTATTCGGGAAAGTTACTCTAAAGCCACAGAC 2246
 QY 1930 CAGCTGCTCCGCTACACCTCTTGGGCAATGACATCCTGGGCTTCTGATGAGGGGCTC 1989
 2247 CAGCTGCTCCGCTACACCTCTTGGGCAATGACATCCTGGGCTTCTGATGAGGGGCTC 2306
 QY 1990 GTCTTCTCGGGCATCAACCTCTACTGCTGCTGATCATCGGGCAAAAGAGTGGCTGTG 2049
 2307 GTCTTCTCGGGCATCAACCTCTACTGCTGCTGATCATCGGGCAAAAGAGTGGCTGTG 2366
 QY 2050 GTGCAGCGCAAGAGAGAGAGAGTCCACCTCGCGCGCGGGGCTTCATGAGCAGCGTACC 2109
 2367 GTGCAGCGCAAGAGAGAGAGAGTCCACCTCGCGCGCGGGGCTTCATGAGCAGCGTACC 2426
 QY 2110 AAGCTCAGGGGCGCTCTTGGGGAGACTCAATCCAAAGACCCAAAGCCGAGGCGCATCTC 2169
 2427 AAGCTCAGGGGCGCTCTTGGGGAGACTCAATCCAAAGACCCAAAGCCGAGGCGCATCTC 2486
 QY 2170 ACGGCACTCATGACCAACAGCGCAAGCTCGCCACTCGCGCAACAGCGCCAAAGATGCTCAT 2229
 2487 ACGGCACTCATGACCAACAGCGCAAGCTCGCCACTCGCGCAACAGCGCCAAAGATGCTCAT 2546
 QY 2230 AAAGCAGACCAAGCAGCAGCTGAGCTCAGCGGCTCCCGCAACCCCAAGAGTCAACCCCAAGC 2289
 2547 AAAGCAGACCAAGCAGCAGCTGAGCTCAGCGGCTCCCGCAACCCCAAGAGTCAACCCCAAGC 2606
 QY 2290 CTGCAGCAGAGCGGAGAGCCAGCCGCGGCAAGCGCGAGTGGGAGAGAGAGCAACCAACCTC 2349
 2607 CTGCAGCAGAGCGGAGAGCCAGCCGCGGCAAGCGCGAGTGGGAGAGAGAGCAACCAACCTC 2666
 QY 2350 ATCAATGCTGACCAAAAGAGCATGCCCCCATGSGGCTCCCTGTGATTCCTCAGCGACCTG 2409
 2667 ATCAATGCTGACCAAAAGAGCATGCCCCCATGSGGCTCCCTGTGATTCCTCAGCGACCTG 2726
 QY 2410 CCCCTGGGGGCTCCCCCAGCAGCATCCCAAGCGTGGTGGGCTCGGCCATCAGCAGCAG 2459
 2727 CCCCTGGGGGCTCCCCCAGCAGCATCCCAAGCGTGGTGGGCTCGGCCATCAGCAGCAG 2786
 QY 2470 GGCTACCAAGCATGAGTACGTGAGCAGCCCAAAATGAGCGAGTGGGCCCAATGCGCGTGTG 2529
 2787 GGCTACCAAGCATGAGTACGTGAGCAGCCCAAAATGAGCGAGTGGGCCCAATGCGCGTGTG 2846
 QY 2530 GAGGAGCAGAGCGCGCAGCAGTGGAGTATTAAGACATCAAGAGCAATCTCAGAGCAGAGAGT 2589
 2847 GAGGAGCAGAGCGCGCAGCAGTGGAGTATTAAGACATCAAGAGCAATCTCAGAGCAGAGAGT 2906
 QY 2590 CCCAAGCATGGGGGAGAGTCTGAGAGTGGAGAGTGGAGAGTGGGCCCAAGAGTTCAGAG 2649
 2907 CCCAAGCATGGGGGAGAGTCTGAGAGTGGAGAGTGGAGAGTGGGCCCAAGAGTTCAGAG 2966
 QY 2650 CGGAGAGCGCTCCCTGGGGTCCCGCGGAGCCTCCCTGCTCTGAGACCGGCTTAAGCAAGCGG 2709
 2967 CGGAGAGCGCTCCCTGGGGTCCCGCGGAGCCTCCCTGCTCTGAGACCGGCTTAAGCAAGCGG 3026
 QY 2710 CTGGAATGACACACTCTCTTCTTACGGGGTTGACTATTAAGAGAGCTACCCCAAGAG 2769

Db 3027 CTGGAATGACACACTCTCTTCTACGGGGTGGACTATTAAGAGAGCTACCCACGAAAC 3086
 QY 2770 TCGCTCAGAGAGAGCCAGCGGACCACTCTCAAAAAGAAACAACTACTCTCTCAAT 2829
 3087 TCGCTCAGAGAGAGCCAGCGGACCACTCTCAAAAAGAAACAACTACTCTCTCAAT 3146
 QY 2830 TCCCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGGAGACAAACCGCGCCGCCCG 2889
 3147 TCCCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGGAGACAAACCGCGCCGCCCG 3206
 QY 2890 CAGAGGGTGAATCTCATCCAGGTGACAGCTCCAGCCTACTGTGGCCAGCGCTGACTGTG 2949
 3207 CAGAGGGTGAATCTCATCCAGGTGACAGCTCCAGCCTACTGTGGCCAGCGCTGACTGTG 3266
 QY 2950 TCGAGGAGCGCCAGCGCTCAACCGCTTACACTGACAGAGTGGGGCTGAAAGCTAGC 3009
 3267 TCGAGGAGCGCCAGCGCTCAACCGCTTACACTGACAGAGTGGGGCTGAAAGCTAGC 3326
 Db 3327 CCTCGCTAAAGCCGAGCTACCCCAACCATCTTTGCTCCCTTCCACATTCATG 3386
 QY 3070 AAGCCCAATGATGGGTGACATA 3093
 3387 AAGCCCAATGATGGGTGACATA 3410

RESULT 4

AAH18729 standard; cDNA; 6060 BP.

ID AAH18729;

AC AAH18729; (first entry)

DE Human cDNA sequence SEQ ID NO:19004.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-316749/34.

PS Claim 8; SEQ ID 19004; 2537bp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX
SQ Sequence 6060 BP; 1639 A; 1526 C; 1363 G; 1532 T; 0 other;

Query Match 96.0%; Score 2969.6; DB 22; Length 6060;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2994; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 96 CAACTATACAAACAGATATCCGGTGTGCGCCCAAGCCGAGGAGGACACACACA 155
DB 1 CAACTATACAAACAGATATCCGGTGTGCGCCCAAGCCGAGGAGGACACACACA 60

QY 156 GAGGACAGAGCTGAGATCCAGATGATATGATCATGAAAGGAAACCTCTACATGTGTC 215
DB 61 GAGGACAGAGCTGAGATCCAGATGATATGATCATGAAAGGAAACCTCTACATGTGTC 120

QY 216 TAGGAGACATATTTACTGTGTATATAGACATCAGACAGGAGAAATTTATGTAG 275
DB 121 TAGGAGACATATTTACTGTGTATATAGACATCAGACAGGAGAAATTTATGTAG 180

QY 276 CAAAAACATGATGAAATCTAGACAGCCGAGATGACATGCAATGGAAGGAAA 335
DB 181 CAAAAACATGATGAAATCTAGACAGCCGAGATGACATGCAATGGAAGGAAA 240

QY 336 ACATAGAGATGAGTGCACAACTTATTAAGTCTCTTAAGAAAAACGATGATGCAT 395
DB 241 ACATAGAGATGAGTGCACAACTTATTAAGTCTCTTAAGAAAAACGATGATGCAT 300

QY 396 GTTTGTGTGGAATATGCTTCAACCTTCTCGAGAAATATAGATGATGAT 455
DB 301 GTTTGTGTGGAATATGCTTCAACCTTCTCGAGAAATATAGATGATGATGAT 360

QY 456 GGAACCATGCGGGGATGAAATTCAGCGGATGGCCAGATGGCCATATGATGCAAAACATGC 515
DB 361 GGAACCATGCGGGGATGAAATTCAGCGGATGGCCAGATGGCCATATGATGCAAAACATGC 420

QY 516 CAAGCTTGCACGTGTTGACAGATGGAATACTAATCTAGCCACAGTGAATCTCTTGC 575
DB 421 CAAGCTTGCACGTGTTGACAGATGGAATACTAATCTAGCCACAGTGAATCTCTTGC 480

QY 576 CATGAGCAGATCATTTACCGGAGTCTTGGAGAAAGCCCTACCTGGGAGCCGCAAGCA 635
DB 481 CATGAGCAGATCATTTACCGGAGTCTTGGAGAAAGCCCTACCTGGGAGCCGCAAGCA 540

QY 636 CGATTCAAAATGGTGAAGAAACCATCTTGTTCAGAGCCGTGATTAACGAGATATAT 695
DB 541 CGATTCAAAATGGTGAAGAAACCATCTTGTTCAGAGCCGTGATTAACGAGATATAT 600

QY 696 CTACTCTTCTTCAGGAAATAGCATGAGATATACACCATGGAAGAGTATGTTTCC 755
DB 601 CTACTCTTCTTCAGGAAATAGCATGAGATATACACCATGGAAGAGTATGTTTCC 660

QY 756 AAGAGTGCATAGTTGTGAAGATGATGATGGAGGATCCTCAAGAGTCCGAGGAACA 815
DB 661 AAGAGTGCATAGTTGTGAAGATGATGATGGAGGATCCTCAAGAGTCCGAGGAACA 720

QY 816 GTGAGCGTGTCTCTGAAGGCGCTGGAATGCTCAATGCTCTGAGAGACTCTATTTTA 875

DB 721 GTGAGCGTGTCTCTGAAGGCGCTGGAATGCTCAATGCTCTGAGAGACTCTATTTTA 780

QY 876 TTTCACATTTCTCCAGGAGATTACAGATGATTCGATACAGGCGGTGATTTGCT 935
DB 781 TTTCACATTTCTCCAGGAGATTACAGATGATTCGATACAGGCGGTGATTTGCT 840

QY 936 GGCACGTTTCTTACACCTTATTAACGATCCCTGGGTCTGAGCTGTGCTTATGACAT 995
DB 841 GGCACGTTTCTTACACCTTATTAACGATCCCTGGGTCTGAGCTGTGCTTATGACAT 900

QY 996 GCTTGACATTTGCCAGTGTTTTCTGAGAGATTCAGGAACAGAAAGTCTCTGATTCAC 1055
DB 901 GCTTGACATTTGCCAGTGTTTTCTGAGAGATTCAGGAACAGAAAGTCTCTGATTCAC 960

QY 1056 CTGAGACACAGTTCTGATGAAAGAGTTCCTAAGCCAGGCGAGTTGTCTGCTGCTC 1115
DB 961 CTGAGACACAGTTCTGATGAAAGAGTTCCTAAGCCAGGCGAGTTGTCTGCTGCTC 1020

QY 1116 ATCCCTCTTGAAGAAATGATGCAACCTCCATGATGATGATGATGATGATGATGATGAT 1175
DB 1021 ATCCCTCTTGAAGAAATGATGCAACCTCCATGATGATGATGATGATGATGATGATGAT 1080

QY 1176 CAAGACGACCCGCTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1235
DB 1081 CAAGACGACCCGCTCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140

QY 1236 GAGAACATGTTGATACCGCTTACCAAAATTCAGTGGACACACACTGCTGGGCATA 1295
DB 1141 GAGAACATGTTGATACCGCTTACCAAAATTCAGTGGACACACACTGCTGGGCATA 1200

QY 1296 TCGAATACACAGTGTGTTTCTGAGATGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1355
DB 1201 TCGAATACACAGTGTGTTTCTGAGATGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260

QY 1356 CAGAAATGAAATAGTGTGTTTCTAATGACAGCTTTCTGAGAGGAGATGAGTGTTTA 1415
DB 1261 CAGAAATGAAATAGTGTGTTTCTAATGACAGCTTTCTGAGAGGAGATGAGTGTTTA 1320

QY 1416 CAACCTCTG -AAAAATGACATATGATGAGTCCAGAACCAAAAGGATATGAGGATGAGGAGC 1474
DB 1321 CAACCTCTGAAAAATGACATATGATGAGTCCAGAACCAAAAGGATATGAGGATGAGGAGC 1380

QY 1475 TGGACAGAGGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1534
DB 1381 TGGACAGAGGAGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440

QY 1535 TTGGCCGTTGTGAACGACATGGAGAGT -AAAAAACTGTATGCTCTCCAGACACCA 1593
DB 1441 TTGGCCGTTGTGAACGACATGGAGAGTAAAAAACTGTATGCTCTCCAGACACCA 1500

QY 1594 TATTGTGATGATTAAGGAAGTGTGCTGCGACCAATTATACCCACAGCAGACTG 1653
DB 1501 TATTGTGATGATTAAGGAAGTGTGCTGCGACCAATTATACCCACAGCAGACTG 1560

QY 1654 ACTTTGAGCAGAGATAGAGCGTGGCAATACAGATGATGATGATGATGATGATGATGATGAT 1713
DB 1561 ACTTTGAGCAGAGATAGAGCGTGGCAATACAGATGATGATGATGATGATGATGATGATGAT 1620

QY 1714 TTTGTGCACTGAATGAGCATTCAGATTCCTCTTCCAGACACACCACTCAGATTCG 1773
DB 1621 TTTGTGCACTGAATGAGCATTCAGATTCCTCTTCCAGACACACCACTCAGATTCG 1680

QY 1774 ACGGCTCAAGAGGGGATGAGTATAGGGGAGGAGATGATGATGATGATGATGATGATGATGAT 1833
DB 1681 ACGGCTCAAGAGGGGATGAGTATAGGGGAGGAGATGATGATGATGATGATGATGATGATGAT 1740

QY 1834 TCACCTGACAGACAGACCCCTTTGGGGAGTGTCTTCCATTAATCACCAAGACAAGAG 1893
DB 1741 TCACCTGACAGACAGACCCCTTTGGGGAGTGTCTTCCATTAATCACCAAGACAAGAG 1800

QY 1894 GGAAGTATGCGGAGAAATTTACTCAAAAGCCACAGACAGTGTGCTGCTGCTGCTGCTG 1953

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Db      1801 GAGGTATTCGGGAAGTACCTCAAGGCGACGACAGCTGTTCCCTCCATCCTCTTG 1860
QY      1954 GCCATTGCAATCTCTGCTTTCGTCATGAGGGGCGCTCTCTCGGGCATACCGTCTAC 2013
      1861 GCCATTGCAATCTCTGCTTTCGTCATGAGGGGCGCTCTCTCGGGCATACCGTCTAC 1920
QY      2014 TGGCTGTGATCATGAGGCGCAAGAGCGTGTGTGTGACGCGCAAGGAGGAGCTC 2073
      1921 TGGCTGTGATCATGAGGCGCAAGAGCGTGTGTGTGACGCGCAAGGAGGAGCTC 1980
Db      2074 ACCCACTGCGCGCGGGGCTCCATGACGAGCGTCCAGCAAGCTCAGCGGCTCTTTGAGGAC 2133
      1981 ACCCACTGCGCGCGGGGCTCCATGAGCAAGCGTCCAGCAAGCTCAGCGGCTCTTTGAGGAC 2040
QY      2134 ACTCAATCCAAAGACCCAAAGCCGAGGCCATCTCAAGCCATCATGCAAAAGCGCAAG 2193
      2041 ACTCAATCCAAAGACCCAAAGCCGAGGCCATCTCAAGCCATCATGCAAAAGCGCAAG 2100
QY      2194 CTGCGCACTCCGCGCAACAGGCGCAAGATGCTCATTTAAAGCAGCAGCAGCAAGCTGAGC 2253
      2101 CTGCGCACTCCGCGCAACAGGCGCAAGATGCTCATTTAAAGCAGCAGCAGCAAGCTGAGC 2160
QY      2254 CTGACGCGCCTCCCAACCCCAAGTCAACCCCAAGCTGACGAGAAAGCCAGC 2313
      2161 CTGACGCGCCTCCCAACCCCAAGTCAACCCCAAGCTGACGAGAAAGCCAGC 2220
QY      2314 CCGGCGACGCGCGCAAGTGGGAGAGGAACCAACCTCTCATTAAGTGTGACAAAGGAGCATG 2373
      2221 CCGGCGACGCGCGCAAGTGGGAGAGGAACCAACCTCTCATTAAGTGTGACAAAGGAGCATG 2280
QY      2374 CCGGCGACGCGCGCAAGTGGGAGAGGAACCAACCTCTCATTAAGTGTGACAAAGGAGCATG 2433
      2281 CCGGCGACGCGCGCAAGTGGGAGAGGAACCAACCTCTCATTAAGTGTGACAAAGGAGCATG 2240
QY      2434 ATCCCAAGCTGTGTGTCTCTGCTCCATCAGCAGAGGCGTCAACAGCATGATGATGATGATG 2493
      2341 ATCCCAAGCTGTGTGTCTCTGCTCCATCAGCAGAGGCGTCAACAGCATGATGATGATGATG 2400
QY      2494 CAGGCGCAAAATGAGCGAGGTGTGCGCCATGAGGTGTGAGGAGGCGCGCGCAGCAGCTGAG 2553
      2401 CAGGCGCAAAATGAGCGAGGTGTGCGCCATGAGGTGTGAGGAGGCGCGCGCAGCAGCTGAG 2460
QY      2554 TATAGACATCAAGAGAACTCTCAGCAGCAAGAGTCCCAACCATGAGGAGTAACTCTGTG 2613
      2461 TATAGACATCAAGAGAACTCTCAGCAGCAAGAGTCCCAACCATGAGGAGTAACTCTGTG 2520
QY      2614 GAGAACTGACAGAGCTTCCGCGCAAGGTTCCAGAGGAGGAGGCTCTCTGAGGAGGCGCGCG 2673
      2521 GAGAACTGACAGAGCTTCCGCGCAAGGTTCCAGAGGAGGAGGCTCTCTGAGGAGGCGCGCG 2580
QY      2674 GAGAGCTGCTCTGTCTCAGAGCGGTCTAAGCAAGCGGCTGAGAAATGCAACACTCTCTTCC 2733
      2581 GAGAGCTGCTCTGTCTCAGAGCGGTCTAAGCAAGCGGCTGAGAAATGCAACACTCTCTTCC 2640
QY      2734 TACGAGGTTGACTATAGAGAGGTACCCACAGAACTCTGTCAGAGAGCCACAGCTCAAGGCC 2793
      2641 TACGAGGTTGACTATAGAGAGGTACCCACAGAACTCTGTCAGAGAGCCACAGCTCAAGGCC 2700
QY      2794 ACCACTTCAAAAGAAACAACTAAGTCTTCAATCTCTCTCAAGCTCTTCCAGAAACAG 2853
      2701 ACCACTTCAAAAGAAACAACTAAGTCTTCAATCTCTCTCAAGCTCTTCCAGAAACAG 2760
QY      2854 AGCTTTGAGAGGAGGAGCAACCGCGCGCGCGCGCGCGAGAGGAGTGAATCTCTCAAGGTG 2913
      2761 AGCTTTGAGAGGAGGAGCAACCGCGCGCGCGCGCGCGAGAGGAGTGAATCTCTCAAGGTG 2820
QY      2914 CACAGCTCCAGAGCTCTGCGCGAGCGCTGACTGTCTGAGGAGAGCCACAGCTCAAGGCC 2973
      2821 CACAGCTCCAGAGCTCTGCGCGAGCGCGTGAATGTCTGAGGAGAGCCACAGCTCAAGGCC 2880
QY      2974 TACAACTCACTGACAGAGGTGAGGAGTGAAGGCTAGCGCTCTGCTTAAAGCGGAGAGTACCC 3033
      2881 TACAACTCACTGACAGAGGTGAGGAGTGAAGGCTAGCGCTCTGCTTAAAGCGGAGAGTACCC 2940

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QY      3034 CCCAACCAATCTCTGCTCCCTTTCACATCCATGAGGCCAATGATGCTGTACATTA 3093
      2941 CCCAACCAATCTCTGCTCCCTTTCACATCCATGAGGCCAATGATGCTGTACATTA 3000
Db
RESULT 5
AAV44295
ID AAV44295 standard; cDNA; 3550 BP.
AC AAV44295;
XX
XX 06-OCT-1998 (first entry)
DE Human secreted protein clone CJ145_1 cDNA.
XX
XX Secreted protein: human fetal brain; nutrition; cytokine; stimulant;
KW cell proliferation; differentiation; immune system; suppressor; ligand;
KW regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW anti-inflammatory; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 126..3053
FT /*tag= a
FT /product= secreted protein
FT /note= "isolated from clone CJ145_1"
XX
XX W09827205-A2.
XX
XX 25-JUN-1998.
XX
XX 17-DEC-1997; 97WO-US23330.
XX
XX 16-DEC-1997; 97US-0991872.
XX 18-DEC-1996; 96US-0769192.
XX 13-JAN-1997; 97US-0783401.
XX
XX (GENE ) GENETICS INST INC.
XX
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racle LA, Spaulding V, Treacy M;
XX
XX WPI: 1998-362774/31.
XX
XX P-PSDB: AAW64221.
XX
XX New polynucleotides and secreted proteins - obtained from human
XX foetal brain, human adult testes, human adult brain and human adult
XX salivary gland cDNA libraries
XX
XX Claim 17a: Page 69-71; 110pp; English.
XX
XX This sequence encodes a novel secreted protein from clone CJ145_1
XX isolated from a human fetal brain cDNA library. This protein has
XX applications for nutritional use, cytokine and cell
XX proliferation/differentiation activity, immune stimulating or
XX suppressing activity, hematopoiesis regulating activity, tissue growth
XX activity, activin/inhibin activity, chemotactic/chemokinetic activity,
XX haemostatic and thrombotic activity, receptor/ligand activity,
XX anti-inflammatory activity, cadherin/tumour invasion suppressor activity,
XX tumour inhibitory activity and other activities.
XX
XX Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;
XX
XX
XX Query Match 88.8%; Score 2746.2; DB 19; Length 3550;
XX Best Local Similarity 94.5%; Pred. No. 0;
XX Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1;
QY 1 ATGAGTCAAGAGCCCTGCTATATATTTACACTGCTACACTTTGCTGGGCTGTTTC 60
      126 ATGAGTCAAGAGCCCTGCTATATTTACACTGCTACACTTTGCTGGGCTGTTTC 185

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QY 61 CCAGAGATTTCAGCCCAATCAGTATTTTCATGGCAGCTATACAAACAGTATCCGGTG 120
 |||||
 Db 186 CCAGAGATTTCAGCCCAATCAGTATTTTCATGGCAGCTATACAAACAGTATCCGGTG 245
 QY 121 TTTTGTGGCCACAGCCAGGAGGAAACCCACACAGAGCCACAGGTGCAGCATCCAGATG 180
 |||||
 Db 246 TTTTGTGGCCACAGCCAGGAGGAAACCCACACAGAGCCACAGGTGCAGCATCCAGATG 305
 QY 181 ATTATGATCATGAGGAAACCCCTCATTTGCTGGTGGAGGACCATTTATATCTGTTGAT 240
 |||||
 Db 306 ATTATGATCATGAGGAAACCCCTCATTTGCTGGTGGAGGACCATTTATATCTGTTGAT 365
 QY 241 ATAGACATCATCACACAGAGAAATTTATTTAGCAAAAAAACTGACATGGAATCTAGA 300
 |||||
 Db 366 ATAGACATCATCACACAGAGAAATTTATTTAGCAAAAAAACTGACATGGAATCTAGA 425
 QY 301 CAGGCCGATGTACACATGACACATGGAAGGAAAAACATPAGATAGTCCCACTTT 360
 |||||
 Db 426 CAGGCCGATGTACACATGACACATGGAAGGAAAAACATPAGATAGTCCCACTTT 485
 QY 361 ATTAAGTTCTTCTAAGAAAAACGATGATGATGCTTTGCTGTGGAATTAATGCTTC 420
 |||||
 Db 486 ATTAAGTTCTTCTAAGAAAAACGATGATGATGCTTTGCTGTGGAATTAATGCTTC 545
 QY 421 AACCTTCCTGCAGAAACTATAAGATGATGATGATGATGATGATGATGATGATGATGAT 480
 |||||
 Db 546 AACCTTCCTGCAGAAACTATAAGATGATGATGATGATGATGATGATGATGATGATGAT 605
 QY 481 GGAATGGCCAGATGCCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 |||||
 Db 606 GGAATGGCCAGATGCCCATATGATGATGATGATGATGATGATGATGATGATGATGAT 665
 QY 541 AAACCTTACCTGACAGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 |||||
 Db 666 AAACCTTACCTGACAGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 725
 QY 601 CTGGAGAGAAACCCCTACCTGCGGACCGTCAGCAGATTCAGAAATGTTGAAAGAACCA 660
 |||||
 Db 726 CTGGAGAGAAACCCCTACCTGCGGACCGTCAGCAGATTCAGAAATGTTGAAAGAACCA 785
 QY 661 TACTTTTTCAGCCGCTGAGTTACGAGATTAATGATGATGATGATGATGATGATGATGAT 720
 |||||
 Db 786 TACTTTTTCAGCCGCTGAGTTACGAGATTAATGATGATGATGATGATGATGATGATGAT 845
 QY 721 GTGAGATATTAACACATGAGGAAAGTATTTTCCCAAGAGTGGCTGAGTGTGTAGAT 780
 |||||
 Db 846 GTGAGATATTAACACATGAGGAAAGTATTTTCCCAAGAGTGGCTGAGTGTGTAGAT 905
 QY 781 GATATGGAGAGATCTCAAGAGTCTGAGAGAACAGTGAACGTGCTTCTGAGAGCCGC 840
 |||||
 Db 906 GATATGGAGAGATCTCAAGAGTCTGAGAGAACAGTGAACGTGCTTCTGAGAGCCGC 965
 QY 841 TTGAGAGTCAGTTCCTGAGAGTCTGATTTTATTTTATTTTCAACATTTCCAGAGCAGTTACA 900
 |||||
 Db 966 TTGAGAGTCAGTTCCTGAGAGTCTGATTTTATTTTATTTTCAACATTTCCAGAGCAGTTACA 1025
 QY 901 GATGATGATGATCAACAGGCGCTGATGTTGCTGAGCAACGTTTCTACACCTTATAC 960
 |||||
 Db 1026 GATGATGATGATCAACAGGCGCTGATGTTGCTGAGCAACGTTTCTACACCTTATAC 1085
 QY 961 AGCATCCCTGGGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1020
 |||||
 Db 1086 AGCATCCCTGGGTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1145
 QY 1021 GGGAGATTCAGAGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1080
 |||||
 Db 1146 GGGAGATTCAGAGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1205
 QY 1081 GTTCTTAAGCCAGGCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1140
 |||||
 Db 1206 GTTCTTAAGCCAGGCCAGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 1265

QY 1141 TCCATGATGCTCCGATGATATCCCTGAGACTTCATCAGACGACCCGCTCATGATGATG 1200
 |||||
 Db 1266 TCCATGATGCTCCGATGATATCCCTGAGACTTCATCAGACGACCCGCTCATGATGATG 1325
 QY 1201 GCAGTCCCTCATCTTCAACAGAGCCATGTTCTGAGAAACAATGTTGATACCCCTT 1260
 |||||
 Db 1326 GCAGTCCCTCATCTTCAACAGAGCCATGTTCTGAGAAACAATGTTGATACCCCTT 1385
 QY 1261 ACCAAATTCAGTGGACACAGCTGCTGGGCCATATCAGATTCACACTGTGTTTCTG 1320
 |||||
 Db 1386 ACCAAATTCAGTGGACACAGCTGCTGGGCCATATCAGATTCACACTGTGTTTCTG 1445
 QY 1321 GGAATCAGAGAGGAGATTCATCTGAGATTTTGGCCAGAAATAGGATGATGTTTCTGA 1380
 |||||
 Db 1446 GGAATCAGAGAGGAGATTCATCTGAGATTTTGGCCAGAAATAGGATGATGTTTCTGA 1505
 QY 1381 AATGACAGCTTTCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
 |||||
 Db 1506 AATGACAGCTTTCCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
 QY 1441 GGAATCAGAGAGAGATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1500
 |||||
 Db 1566 GGAATCAGAGAGAGATTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1625
 QY 1501 GTTGGCTTCTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
 |||||
 Db 1626 GTTGGCTTCTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1685
 QY 1561 TGTAAAAAAACCTGTATTGCTCCAGAGACCATATTTGATGATGATGATGATGATGATGAT 1620
 |||||
 Db 1686 TGTAAAAAAACCTGTATTGCTCCAGAGACCATATTTGATGATGATGATGATGATGATGAT 1745
 QY 1621 GCCTGACCCATTTATACCCACAGAGACTGATTTTGAAGAGACATAGAGCCGTG 1680
 |||||
 Db 1746 GCCTGACCCATTTATACCCACAGAGACTGATTTTGAAGAGACATAGAGCCGTG 1805
 QY 1681 AATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 |||||
 Db 1806 AATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1853
 QY 1741 TCCCTTGTGCCAGACACACCATGATTCAGAGGCTCAAGAGGGGATAGATCTAGG 1800
 |||||
 Db 1854 TCCCTTGTGCCAGACACACCATGATTCAGAGGCTCAAGAGGGGATAGATCTAGG 1853
 QY 1801 GGAAGATGCTGAGACTGGAAGCATCTGCTGACTCAGCTGACAGACAGACCTTTGGGG 1860
 |||||
 Db 1854 TCCCTTGTGCCAGACACACCATGATTCAGAGGCTCAAGAGGGGATAGATCTAGG 1853
 QY 1861 GCACTGTCTTCCATTAATCAACAGACAGAGAGGAGTATTCGGGAAAGTTACTCTAAA 1920
 |||||
 Db 1854 TCCCTTGTGCCAGACACACCATGATTCAGAGGCTCAAGAGGGGATAGATCTAGG 1880
 QY 1921 GGCACGACACAGCTGATGCTCCGCTGACCTCTTGGGCAATGAGATCATCTCGCTTGGTC 1980
 |||||
 Db 1881 GGCACGACACAGCTGATGCTCCGCTGACCTCTTGGGCAATGAGATCATCTCGCTTGGTC 1940
 QY 1981 ATGGGGGCGCTCTCTGGGGATCAGCGTACAGCGCTCTGATGATGATGATGATGATGATGAT 2040
 |||||
 Db 1941 ATGGGGGCGCTCTCTGGGGATCAGCGTACAGCGCTCTGATGATGATGATGATGATGATGAT 2000
 QY 2041 GTGGCTGTGTGACAGCGCAAGAGAGAGTCAACCACTGCGCGCGGGGCTCCATGAGC 2100
 |||||
 Db 2001 GTGGCTGTGTGACAGCGCAAGAGAGAGTCAACCACTGCGCGCGGGGCTCCATGAGC 2060
 QY 2101 AGCGTACCAAGCTCAGCGGCTCTTGGGAGACACTCATCAATCAAAAGACCCAAAGCCGAG 2160
 |||||
 Db 2061 AGCGTACCAAGCTCAGCGGCTCTTGGGAGACACTCATCAATCAAAAGACCCAAAGCCGAG 2120
 QY 2161 GCAATCTCAGCGCACTATGACAGAGGCAAGCTCGGCACTCCCGGGAACAGGCGCAAG 2220
 |||||
 Db 2121 GCAATCTCAGCGCACTATGACAGAGGCAAGCTCGGCACTCCCGGGAACAGGCGCAAG 2180
 QY 2221 ATGCTCAATTAAGACAGACCAACCACTGAGCTGAGCGGCTCCCAACCCAGAGTCA 2280

Db	2181	ATGCTATTAAACGACAGACGACCGACCTTGACGGCCCTCCCGACCCAGAGTCA	2240
QY	2281	ACCCCAACGCTGGAGCAGAAAGCGAAAGCCAGCCGCGGACGCCGAGTGGAGAGAAAC	2340
Db	2241	ACCCCAACGCTGCAGCAGAAAGCGAAAGCCAGCCGCGGACGCCGAGTGGAGAGAAAC	2300
QY	2341	CAGAACCTCATCAATACCTCTGACACAAAGGACATCCCCCATGSGGCTCCCTGTGATTCGC	2400
Db	2301	CAGAACCTCATCAATGCTGTGCACAAAGGACATCCCCCATGSGGCTCCCTGTGATTCGC	2360
QY	2401	ACGGAACCTGGCCCTGGGCGGCTCCCGACGACATCCCGCAGCTGGTGGCTCTGCCATC	2460
Db	2361	ACGGAACCTGGCCCTGGGCGGCTCCCGACGACATCCCGCAGCTGGTGGCTCTGCCATC	2420
QY	2461	ACCGAGCAGGGGCTACGACGATGAGTACGTGGAGACCCCAAAATGAGCAGATGGCCAG	2520
Db	2421	ACCGAGCAGGGGCTACGAGCATGAGTACGTGGAGACCCCAAAATGAGCAGATGGCCAG	2480
QY	2521	ATGGCGCTGGAGAGCAGCAGGCCGCGACACACTGGAGTATTAAGACATCAAGAAACATTCACG	2580
Db	2481	ATGGCGCTGGAGAGCAGCAGGCCGCGACACACTGGAGTATTAAGACATCAAGAAACATTCAGC	2540
QY	2581	AGCAAGAGTCCCAACCATGGGGGTGAACCTTGTGGAGAACCTGGACACCTGCCGCCCAAA	2640
Db	2541	AGCAAGAGTCCCAACCATGGGGGTGAACCTTGTGGAGAACCTGGACACCTGCCGCCCAAA	2600
QY	2641	GTTCACAGAGGCGGAGGCGCTCCCTGGGTCCCGCGGAGCCTCCCTGTCTCAGACCGGTCTA	2700
Db	2601	GTTCACAGAGGCGGAGGCGCTCCCTGGGTCCCGCGGAGCCTCCCTGTCTCAGACCGGTCTTA	2660
QY	2701	AGCAAGGCGGTGGAATAATGACACCACTCCTCTTCTCTAGGCGGGGTGTACTATAAGAGAGCTAC	2760
Db	2661	AGCAAGGCGGTGGAATAATGACACCACTCCTCTTCTCTAGGCGGGGTGTACTATAAGAGAGCTAC	2720
QY	2761	CCCAAGAACTGGCTACAGAGAACGCCACAGGCCACCACTCTCAAAAGAAACCAACCTAAC	2820
Db	2721	CCCAAGAACTGGCTACAGAGAACGCCACAGGCCACCACTCTCAAAAGAAACCAACCTAAC	2780
QY	2821	TGCTCCAAATCTCTCACTCTCCAGAAACCAAGCTTTGGCAGGGGAGACAAACCCGCG	2880
Db	2781	TGCTCCAAATCTCTCACTCTCCAGAAACCAAGCTTTGGCAGGGGAGACAAACCCGCG	2840
QY	2881	CCCGCCCCCGAGAGGGTGGACTCCATCCAGGTGAGACAGCTCCAGACATCTGGCCAGGCG	2940
Db	2841	CCCGCCCCCGAGAGGGTGGACTCCATCCAGGTGAGACAGCTCCAGACATCTGGCCAGGCG	2900
QY	2941	GTGACTGTCTGTGAGGAGCAGCCAGCCTCAAGCCTTACAACCTCACTGACAAAGGTGGGGCTG	3000
Db	2901	GTGACTGTCTGTGAGGAGCAGCCAGCCTCAAGCCTTACAACCTCACTGACAAAGGTGGGGCTG	2960
QY	3001	AAGCGTACGCGCTCGCTAAAGCCGAGCTACCCCGCAAAACCATCTTTGCTCCCTTTC	3060
Db	2961	AAGCGTACGCGCTCGCTAAAGCCGAGCTACCCCGCAAAACCATCTTTGCTCCCTTTC	3020
QY	3061	ACATCCATGAAAGCCCATGATGTCGTGACATTA	3093
Db	3021	ACATCCATGAAAGCCCATGATGTCGTGACATTA	3053
RESULT 6			
AAF98469			
ID	AAF98469 standard; cDNA; 3550 BP.		
XX	AAF98469;		
AC			
XX			
DT	07-JUN-2001 (first entry)		
XX			
DE	Human cDNA clone CJ145.1 sequence SEQ ID 160.		
XX			
KW	Human; secreted protein; nutrient; cytokine modulator; proliferatin;		
KW	differentiation; immune system modulator; tissue growth; chemotactic;		
KW	haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;		

XX	haematopoiesis.
OS	Homo sapiens.
PN	W0200119986-A1.
XX	
PD	22-MAR-2001.
XX	
PF	14-SEP-2000; 2000WO-US25135.
XX	
PR	17-SEP-1999; 99US-0398829.
XX	
PA	(GENY) GENETICS INST INC.
PI	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI	Meberberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX	
DR	WI: 2001-244601/25.
XX	P-PSDB: AAB90731.
PT	Isolated nucleic acids encoding polypeptides, useful for modulating
PT	p.g. cytokine and cell proliferation/differentiation activity, the
PT	immune system and haematopoiesis regulating activity -
PS	Disclosure: Page 486-487; 557pp; English.
XX	
CC	Human cDNA clones represented in AAP98374 - AAP98489 encode secreted
CC	proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC	tissue types, and may be used in the prevention, treatment and diagnosis
CC	of diseases associated with inappropriate protein expression. The
CC	polypeptides and nucleic acids may be used as nutrients or to modulate
CC	cytokine and cell proliferation/differentiation activity and may also be
CC	involved in modulation of the immune system. The cDNA sequences,
CC	proteins, their agonists and/or antagonists exhibit haematopoiesis
CC	regulating activity; tissue growth activity; activin/inhibin activity;
CC	chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC	activity; receptor/ligand activity; anti-inflammatory activity;
CC	haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC	tumour inhibition activity. Included in the invention are probes
CC	represented in AAP98490 - AAP98572 which are specific for the cDNA clones
CC	encoding the secreted proteins.
SQ	Sequence 3550 BP: 957 A; 994 C; 856 G; 742 T; 1 other:
	Query Match 88.8%; Score 2746.2; DB 22; Length 3550;
	Best Local Similarity 94.5%; Pred. No. 0;
	Matches 2923; Conservative 1; Mismatches 4; Indels 165; Gaps 1
OY	1 ATGAGGTGAGAAGCCTTGCTGCTATATTTCACACTGCTCACTTTGCTGGGCGTGTTC 60
DB	
OY	126 ATGAGGTGAGAAGCCTTGCTGCTATATTTCACACTGCTCACTTTGCTGGGCGTGTTC 185
DB	
OY	61 CCAGAAGATTTCGAGCGCATCGATGTAATTTGGCATGGCACTATACAAACATATCCGGTG 120
DB	
OY	186 CCAGAAGATTTCGAGCGCAATCATGATTTTGCATGGCACTATACAAAACATATCCGGTG 245
DB	
OY	121 TTGTGGGGCCACAAGGCCAAGAGGAACACCACACAGAGGCGACGCTGCACATCCAGATG 180
DB	
OY	246 TTGTGGGGCCACAAGGCCAAGAGGAACACCACACAGAGGCGACGCTGCACATCCAGATG 305
DB	
OY	181 ATTATGATCATGAAGCGAACCCCTTCATTTGCTGCTAGGAGCACATTTATATCTGTGAT 240
DB	
OY	306 ATTATGATCATGAAGCGAACCCCTTCATTTGCTGCTAGGAGCACATTTATATCTGTGAT 365
DB	
OY	241 ATTAGACATCMCACACACGGAAGAAATTATTTAGACAAAAAATCGACATGGAATCTAG 3000
DB	
OY	366 ATTAGACATCMCACACACGGAAGAAATTATTTAGACAAAAAATCGACATGGAATCTAG 425
DB	
OY	301 CAGGCGCAGATGACACATGACAGATGAAGGAAAAACATTAAGATGATGCCAACTTT 360
DB	
OY	426 CAGGCGCAGATGACACATGACAGATGAAGGAAAAACATTAAGATGATGCCAACTTT 485
DB	
OY	361 ATTTAAAGTCTCTTAAAGAAAAACGATGATGATTTTGTGCTGTGGAACATAATGCTTTC 420

QY	258	AGCAAGAGTCCCAACCATGGGGGAGAACTTTGTGGAGAACTTGGACACTGCCCCAAA	2640
Db	2541	AGCAAGAGTCCCAACCATGGGGGAGAACTTTGTGGAGAACTTGGACACTGCCCCAAA	2600
QY	2641	GTTCACAGAGGAGGAGGCTCCCTGGGTCCCGGGAGACTTCCTGTCTAGACCCGCTCA	2700
Db	2601	GTTCACAGAGGAGGAGGCTCCCTGGGTCCCGGGAGACTTCCTGTCTAGACCCGCTTCA	2660
QY	2701	AGCAAGCGGCTGGAAATGCACACTCTCTTCTCCAGGGGTGACTATAAAGAGGTAC	2760
Db	2661	AGCAAGCGGCTGGAAATGCACACTCTCTTCTCCAGGGGTGACTATAAAGAGGTAC	2720
QY	2761	CCGACGAAGTGGCTCAGAGAGAAAGCCACAGGCCACCACTCTCAAAAGAAACACATAC	2820
Db	2721	CCGACGAAGTGGCTCAGAGAGAAAGCCACAGGCCACCACTCTCAAAAGAAACACATAC	2780
QY	2821	TTCCTCCAAATTCCTCTACACGCTCTCCAGAAACCCAGAGCTTTGGCAGGGGAGCAACCCGGC	2880
Db	2781	TTCCTCCAAATTCCTCTACACGCTCTCCAGAAACCCAGAGCTTTGGCAGGGGAGCAACCCGGC	2840
QY	2881	CCGCCCCCGAGAGAGGTGGAATCCATCCATCAGGTGCACACCTCCAGCATCTGTGGCCAGCC	2940
Db	2841	CCGCCCCCGAGAGAGGTGGAATCCATCCATCAGGTGCACACCTCCAGCATCTGTGGCCAGCC	2900
QY	2941	GTGACTGTCTTCGAGGACAGCCAGGCTCAAGGCTCAACACTACGACACAGGTGGGGGCTG	3000
Db	2901	GTGACTGTCTTCGAGGACAGCCAGGCTCAAGGCTCAACACTACGACACAGGTGGGGGCTG	2960
QY	3001	AAGGTACGCGCCTCGCTAAAGCCCGAGCTACCCCCAAACCATCTTTGTCCCTTTCC	3060
Db	2961	AAGGTACGCGCCTCGCTAAAGCCCGAGCTACCCCCAAACCATCTTTGTCCCTTTCC	3020
QY	3061	ACATTCATGAAGCCCAATGATGCGGTGATCAATA	3093
Db	3021	ACATTCATGAAGCCCAATGATGCGGTGATCAATA	3053

RESULT 7
AAA93618
ID AAA93618 standard; DNA; 3333 BP.

AC AAA93618;

DT 16-JAN-2001 (first entry)

DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA

KW SEX protein, human; secreted; membrane-associated; cancer;
 KW proliferation regulator; differentiation regulator; non-malignant tumour
 KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS
 KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
 KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
 KW neurological disease; Alzheimer's disease; trauma; wounding;
 KW spinal cord injury; skeletal disorder; cystostatic; immunosuppressive;
 KW anti-HIV; antiinflammatory; antirheumatic; antiarteriosclerotic;
 KW neuroprotective; vulnerable; antiallergic; antimicrobial; cardiant;
 KW dermatological; gene therapy; ds.

OS Homo sapiens

PN W0200053742-A2.

PD 14-SEP-2000

PF 09-MAR-2000; 2000WO-US06280

PR 09-MAR-1999; 99US-0123667

XX
XX
XXXXX COMPANY

XX
XX

PI Shimkets RA;

DR	XX		WP1: 2000-594318/56.
DR	XX	P-PSDB; AAB23031.	
PT	XX	Novel human membrane associated or secreted polypeptides and	
PT	XX	polynucleotides useful for diagnosis, prevention and treatment of	
PT	XX	pathological states such as cancer, immune, cardiovascular and	
PT	XX	neurological disorders	
PS	PS	Claim 3; Fig 3; 151pp; English.	
CC	CC	Sequences AAA93616-7A93631 and AAA93673-7A93676 represent nucleic acids	
CC	CC	which encode human SECX proteins (BAB23029-B23048). The SECX proteins	
CC	CC	of the invention are either secreted or membrane-associated proteins	
CC	CC	and act as regulator of cellular proliferation and differentiation. SECX	
CC	CC	proteins or nucleotides are useful for diagnosing the presence of, or	
CC	CC	predisposition to, a disease associated with altered levels of SECX	
CC	CC	proteins and nucleotides. The SECX proteins are also useful to screen	
CC	CC	compounds that modulate SECX activity or expression. The interaction of	
CC	CC	a SECX protein with other cellular proteins may be useful to modulate	
CC	CC	the activity of a partner protein, cellular proliferation, cellular	
CC	CC	differentiation and cell survival. SECX nucleotides are useful for the	
CC	CC	recombinant expression of SECX protein, and may be used detect SECX mRNA	
CC	CC	or genetic lesions in the SECX gene. They may also be used to modulate	
CC	CC	SECX expression (e.g., using antisense oligonucleotides). SECX nucleic	
CC	CC	acid sequences are also useful for identifying a cell or tissue type in	
CC	CC	a biological sample, and in forensic biology. SECX primers or probes are	
CC	CC	useful for detecting for contamination. Diseases that may be treated or	
CC	CC	tissue cultures for contamination. Diseases that include cancer (e.g.,	
CC	CC	colorectal carcinoma, prostate cancer), benign tumours, immune disorders	
CC	CC	(including autoimmune diseases, transplant rejection, allergies, AIDS),	
CC	CC	infections, inflammatory disorders, arthritis, haematopoietic disorders,	
CC	CC	skin disorders, cardiovascular disorders, atherosclerosis, stenosis,	
CC	CC	neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,	
CC	CC	surgical or traumatic wounds, spinal cord injury), and skeletal	
CC	CC	disorders.	
SQ	SQ	Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 1 other;	
		Query Match 87.2%; Score 2698; DB 21; Length 3333;	
		Best Local Similarity 93.9%; Pred. No. 0;	
		Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3	
OY	1	ATGAGGTCTCGAAGCCTTGGCTGCTATTATTTACACACTGCTCACTTTGCTGGGCTGGTTTC	60
Db	214	ATGAGGTCTCGAAGCCTTGGCTGCTATTATTTACACACTGCTCACTTTGCTGGGCTGGTTTC	273
OY	61	CCAGAAGATTTCGAGCCAACTACAGTATTTTGCGATGGCACTATTAACAACAGTATCCGGNG	120
Db	274	CCAGAAGATTTCGAGCCAACTACAGTATTTTGCGATGGCACTATTAACAACAGTATCCGGNG	333
OY	121	TTTTGGGGCCACAAGCCAGACGAGAACACCACACAGACGACACAGGCTGGACATCCAGATG	180
Db	334	TTTTGGGGCCACAAGCCAGACGAGAACACCACACAGACGACACAGGCTGGACATCCAGATG	393
OY	181	ATTATGATCATGAAGCGAAACCCCTTACATTGCTGCTAGGAGCACATATTTATCTGTGAT	240
Db	394	ATTATGATCATGAAGCGAAACCCCTTACATTGCTGCTAGGAGCACATATTTATCTGTGAT	453
OY	241	ATRAGACACMCMCACACGGGAAGAAATTTWTGTAGCAAAAAAAATGCATGGAATCTTAGA	3000
Db	454	ATRAGACACATCACACACGGGAAGAAATTTATTGTAGCAAAAAAAATGCATGGAATCTTAGA	5133
OY	301	CAGGCCGATGTAGACACATGACAGATGAAGGGAATAACATPAGATGAGTGCACAACTT	360
Db	514	CAGGCCGATGTAGACACATGACAGATGAAGGGAATAACATPAGATGAGTGCACAACTT	573
OY	361	ATTAAAGTCTTTTAAAGAAAACGATGATGATTTGTTGTCTGTGGAACTATAGCTTTC	420
Db	574	ATTAAAGTCTTTTAAAGAAAACGATGATGATTTGTTGTCTGTGGAACTATAGCTTTC	633
OY	421	AACCCCTTCGCGAAGAACTATAAGATGATGATTCATTTGGAACCAATTCGGGGATGAAITTCAC	480

Db 634 AACCTCTCTGAGAACTATAGATGATACATTGAAACCATGCGGGATTAATTCAGC 693
 QY 481 GGAATGGCCAGATGGCCATATGATGCAACATGCAACGTGCACTGTTGCAATGGA 540
 Db 694 GGAATGGCCAGATGGCCATATGATGCAACATGCAACGTGCACTGTTGCAATGGA 753
 QY 541 AACTATATCTAGCCACAGTGAATGATCTCTGCAATGAGCAGTCAATTTCCGGAGT 600
 Db 754 AACTATATCTAGCCACAGTGAATGATCTCTGCAATGAGCAGTCAATTTCCGGAGT 813
 QY 601 CTGGAGAAAGCCCTTACCTCGGACCGTCAAGCAGATTCAAATGTTGAAAGACCA 660
 Db 814 CTGGAGAAAGCCCTTACCTCGGACCGTCAAGCAGATTCAAATGTTGAAAGACCA 873
 QY 661 TACTTGTTCAGACCGGTGATTAAGAGATATATCTACTCTCTTCGAGAAATAGCA 720
 Db 874 TACTTGTTCAGACCGGTGATTAAGAGATATATCTACTCTCTTCGAGAAATAGCA 933
 QY 721 GTGAGATATACACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 780
 Db 934 GTGAGATATACACCATGAGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGAAGAT 993
 QY 781 GATATGGAGATGATCAAGAGTCTCGAGAAACAGTGAACGTGCTCTGAGAGGCGGC 840
 Db 994 GATATGGAGATGATCAAGAGTCTCGAGAAACAGTGAACGTGCTCTGAGAGGCGGC 1053
 QY 841 TTGAATGCTCAGTCTCCTGAGAGACTCTATTTTATTTCAAGATTCGACAGGAGTTAA 900
 Db 1054 TTGAATGCTCAGTCTCCTGAGAGACTCTATTTTATTTCAAGATTCGACAGGAGTTAA 1113
 QY 901 GATGATATGATCAACGCGGCTGATGTTGCTCGGCAAGTTTCTACCTTTATAC 960
 Db 1114 GATGATATGATCAACGCGGCTGATGTTGCTCGGCAAGTTTCTACCTTTATAC 1173
 QY 961 AGCATCCCTGGGTCTGAGTCTGCTGATGACATCTTGACATTCGACAGTGTGTTTACT 1020
 Db 1174 AGCATCCCTGGGTCTGAGTCTGCTGATGACATCTTGACATTCGACAGTGTGTTTACT 1233
 QY 1021 GGGAGATTCAGAGAACAGAGTCTGATTCACCTGAGACACAGTTCCTGATGAACGA 1080
 Db 1234 GGGAGATTCAGAGAACAGAGTCTGATTCACCTGAGACACAGTTCCTGATGAACGA 1293
 QY 1081 GTTCTCAAGCCGAGGCGAGTGTGCTGCTGCTGCTCACTCTTGAAGATATGCAACC 1140
 Db 1294 GTTCTCAAGCCGAGGCGAGTGTGCTGCTGCTGCTCACTCTTGAAGATATGCAACC 1353
 QY 1141 TCCAAATGATTCCTGATGATACCTGATCACTATCAGACGACCGGCTCATGATGAG 1200
 Db 1354 TCCAAATGATTCCTGATGATACCTGATCACTATCAGACGACCGGCTCATGATGAG 1413
 QY 1201 GCAATGCTCCATCTTCAACAGGCGCATGTTCTCTGAGAACATGTCATACCCGCTT 1260
 Db 1414 GCAATGCTCCATCTTCAACAGGCGCATGTTCTCTGAGAACATGTCATACCCGCTT 1473
 QY 1261 ACCAAATTCGAGTGAACAGTCTGCTGGGCGCATATGAAATCACTGAGTGTGTTCTG 1320
 Db 1474 ACCAAATTCGAGTGAACAGTCTGCTGGGCGCATATGAAATCACTGAGTGTGTTCTG 1533
 QY 1321 GGATCAGAGAGGAAATCATCTGAAAGTGTGTTGCGCAGATAGGAAATAGTGTGTTCTA 1380
 Db 1534 GGATCAGAGAGGAAATCATCTGAAAGTGTGTTGCGCAGATAGGAAATAGTGTGTTCTA 1593
 QY 1381 AATGACAGCCCTTTTCTGAGAGAGATAGTGTGTTTACAACCTCTGAAAAATGCACTATGAT 1440
 Db 1594 AATGACAGCCCTTTTCTGAGAGAGATAGTGTGTTTACAACCTCTGAAAAATGCACTATGAT 1653
 QY 1441 GGAATGCAAGCAAAAGATATGAGGATGATGATGATGATGATGATGATGATGATGAT 1500
 Db 1654 GGAATGCAAGCAAAAGATATGAGGATGATGATGATGATGATGATGATGATGATGAT 1713
 QY 1501 GTTCGATCTCTACTGTTGTGATTAAGTTCCTCTGCGGCTGTAACGACATGGAGAG 1560

Db 1714 GTTCGATCTCTACTGTTGTGATTAAGTTCCTCTGCGGCTGTAACGACATGGAGAG 1773
 QY 1561 TGTAAAAAAACCTGATTTGCTCCAGAGACCCATATGATGATGATTAAGAGAGTGGT 1620
 Db 1774 TGTAAAAAAACCTGATTTGCTCCAGAGACCCATATGATGATGATTAAGAGAGTGGT 1833
 QY 1621 GCTTCGACGATTTTATCACCCCAAGCAGACACTGTTTGAACAGACATAGAGGTGGC 1680
 Db 1834 GCTTCGACGATTTTATCACCCCAAGCAGACACTGTTTGAACAGACATAGAGGTGGC 1893
 QY 1681 AATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
 Db 1894 AATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1941
 QY 1741 TCCCTCTTGGCCAGACAAACCATCAGATTCAGAGGCTCAAGAGGGGATAGTGTAGG 1800
 Db 1942 ----- 1941
 QY 1801 GAGAGATGCTGAGTGAAGATCTGTTGACTACCTGACAGACAGACCTTTGGGG 1860
 Db 1942 ----- 1941
 QY 1861 GAGTGTCTCCCATATCAACCAAGCAAGAGAGATGATTCGGAAAGTTTACTCAAA 1920
 Db 1942 ----- GAGTGTATTCGGAAAGTTTACTCAAA 1968
 QY 1921 GGGCAGACAGAGTGGTTCCCGTACCCGCTTTGGGCTGATGATGATGATGATGATGAT 1980
 Db 1969 GGGCAGACAGAGTGGTTCCCGTACCCGCTTTGGGCTGATGATGATGATGATGATGAT 2028
 QY 1981 ATGGGGGCGGCTTCTCGGAGCATCACCGTCTACTGCTGTGATCATGCGGCGCAAAAG 2040
 Db 2029 ATGGGGGCGGCTTCTCGGAGCATCACCGTCTACTGCTGTGATCATGCGGCGCAAAAG 2088
 QY 2041 GTGGCTGTGATGAGCGCAAGAGAGAGTCAACCACTGCGGCGGCGGCTCATGAGAG 2100
 Db 2089 GTGGCTGTGATGAGCGCAAGAGAGAGTCAACCACTGCGGCGGCGGCTCATGAGAG 2148
 QY 2101 AGGCTACCAAGCTCAGCGGCTCTTTGGGAGACTCAATCCAAAGCCCAAGCCGAGAG 2160
 Db 2149 AGGCTACCAAGCTCAGCGGCTCTTTGGGAGACTCAATCCAAAGCCCAAGCCGAGAG 2208
 QY 2161 GCCATCTCAGCGCTCATGATGACCAACAGCGAGTGGCTGCGGCAACAGGCTCAAG 2220
 Db 2209 GCCATCTCAGCGCTCATGATGACCAACAGCGAGTGGCTGCGGCAACAGGCTCAAG 2268
 QY 2221 ATGCTCATTTAAAGCAGACCGACCACTGAGTGGCTGCGGCTGCGGCAACAGGCTCA 2280
 Db 2269 ATGCTCATTTAAAGCAGACCGACCACTGAGTGGCTGCGGCTGCGGCAACAGGCTCA 2328
 QY 2281 ACCCAACGCTGAGCAGAGCGGAGCCGAGCGGCGGAGCCGAGTGGGAGAGAGAAC 2340
 Db 2329 ACCCAACGCTGAGCAGAGCGGAGCCGAGCGGCGGAGCCGAGTGGGAGAGAGAAC 2388
 QY 2341 CAGAACTCATCAATGCTGTGACAAAGAGACATGCCCCCATGGGCTCCCTGTGATTCGC 2400
 Db 2389 CAGAACTCATCAATGCTGTGACAAAGAGACATGCCCCCATGGGCTCCCTGTGATTCGC 2448
 QY 2401 ACGGACCTGCCCCGCGGGGCTCCCGAGCCATCCCAAGCGGAGTGGTGTGCTGCCATC 2460
 Db 2449 ACGGACCTGCCCCGCGGGGCTCCCGAGCCATCCCAAGCGGAGTGGTGTGCTGCCATC 2508
 QY 2461 ACGGACGAGGCTTACCGACATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
 Db 2509 ACGGACGAGGCTTACCGACATGATGATGATGATGATGATGATGATGATGATGATGAT 2568
 QY 2521 ATGGCGCTGAGAGACAGCGCGCACACTGAGATTAAGACCATCAAGAGAGATCTAGC 2580
 Db 2569 ATGGCGCTGAGAGACAGCGCGCACACTGAGATTAAGACCATCAAGAGAGATCTAGC 2628
 QY 2581 AGCAAGATTCACCAACATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2640
 Db 2629 AGCAAGATTCACCAACATGAGGATGATGATGATGATGATGATGATGATGATGATGAT 2688

QY	2641	GTTCACACGCGGGAGGCGCTCCCTGCGTCCCCCGGAGACCTCCTCCTGTCACAGCCGGCTCTA	2700
Db	2689	GTTCACACGCGGGAGGCGCTCCCTGCGTCCCCCGGAGACCTCCTCCTGTCACAGCCGGCTCTA	2748
QY	2701	AGCAAGCGGGCTGGAAATATGCACACACTCTCTCTCTACAGGGGTGACTTTAAGAGAGCTAC	2760
Db	2749	AGCAAGCGGGCTGGAAATATGCACACACTCTCTCTCTACAGGGGTGACTTTAAGAGAGCTAC	2808
QY	2761	CCACAGAACTGCTACAGAGAAAGCCACAGGCCAC- ACTCTCAAAAGAAACAACACTAA	2819
Db	2809	CCACAGAACTGCTACAGAGAAAGCCACACTGACCTCACTCTCACTCAAGAAACAACACTAA	2868
QY	2820	CTCTCCAACTCCCTCTC- ACCCTCCGAGAAACCGAGAGCTTGGAGAGGGAGACAAACCGC	2878
Db	2869	CCCCGACAACTTCACCTTGACTTTCAAAGGGACCAAGAGTTTGGAGAGGGAGACAAACCGC	2928
QY	2879	CGCCCGCCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCCATCTGGCCAGG	2938
Db	2929	CGCCCGCCCGCCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCAGCCCATCTGGCCAGG	2988
QY	2939	CCGTGACTGTCTCGAGGAGGCCGACGCTCAACGGCTTACAATCTCTGACAAGTCCGGGGC	2998
Db	2989	CCGTGACTGTCTCGAGGAGGCCGACGCTCAACGGCTTACAATCTCTGACAAGTCCGGGGC	3048
QY	2999	TGAAGCGTACGCCCTCGCTTAAAGCGGAGCGTACCCCCCAAAACCAATCCTTTGCTCCCTTT	3058
Db	3049	TGAAGCGTACGCCCTCGCTTAAAGCGGAGCGTACCCCCCAAAACCAATCCTTTGCTCCCTTT	3108
QY	3059	CCACATCATTAAGACCCCAATGATGCGGTAACTAA	3093
Db	3109	CCACATCATTAAGACCCCAATGATGCGGTAACTAA	3143

XX	RESULT 7
XX	AA568807
XX	ID AA568807 standard; cDNA; 3039 BP.
XX	AA568807;
XX	13-FEB-2002 (first entry)
XX	DNA encoding novel human diagnostic protein #4611.
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss
XX	Homo sapiens.
XX	WO200175067-A2.
XX	11-OCT-2001.
XX	30-MAR-2001; 2001WO-US08631.
XX	31-MAR-2000; 2000US-0540217.
XX	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSEQ INC.
XX	Drmnac RT, Liu C, Tang YT;
XX	WPI: 2001-639362/73.
XX	P-PSDB; ABG04620.
XX	New isolated polynucleotide and encoded polypeptides, useful in
XX	diagnostics, forensics, gene mapping, identification of mutations
XX	responsible for genetic disorders or other traits and to assess
XX	biodiversity -
XX	Claim 1: SEQ ID No 4611; 103pp: English.
XX	The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes.
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/publ/published_pct_sequences.

Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;

Query Match	71.8%	Score 2221.8	DB 23	Length 3039
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Best Local Similarity	91.26;	Freq. NO. 0;
Matches 2408; Conservative	0;	Mismatches 167; Indels 66; Gaps 2;

Matches	2408;	Conservative	0;	Mismatches	167;	Indels	66;	Gaps	47;
---------	-------	--------------	----	------------	------	--------	-----	------	-----

519 CGTGCAC TGTTCAGATGGAAACTATACTCAGCCACAGTGACTGACTTCCTTGGCAT 578

Db 399 CCTGACTCTGTTCTCCAGATGGAACACTATATACTCAGCCACAGTGACTGACTTCTTGGCAT 458

579 TGACGAGTCAATTACCGGAGTCTTGAGAAAGCCCTACCTGCGGACCGTCAAGCAGCA 638

Db 459 TGACGAGTCATTACCGGAGTCTTGAGAAAGCCCTACCTGCGGACCGTCAAGCAGCA 518

639 TTCAAATGGTTGAAGAACCATACCTTTGTTCAAGCCGTGGATTACGGAGATTATATCTA 698

Db 519 TTCAAATGGTTGAAGAACCATTCTTGTTCACGCCGTGGATTACGGAGATTATCTA 578

699 CTTCTTCTCAGGGAATAGCAGTGGAGTATAACACCATGGGAAGTATTCCCAAG 758

579 CTTCTTCTCAGGGAATAGCAGTGGAGTATAACACCATGGGAAGTAGTTTCCCAAG 638

759 AGTGGCTCAGGTTTGTAAGATGATATGGGAGGATCTCAAGAGTCCCTGGAGAACACTG 818

639 AGTGGCTCAGGTTTGTAAAGATGATATGGGAGGATCTCAAGAGTCCCTGGAGAACAGTG 698

819 GACGTCCTCTGAAGCGCGCTTGAACCTGCTCAGTTCCTGGAGACTCTCATTTTATT 878

699 GACGTCCTGAGGGCGCTTGAACCTGCTCAGTCCCTGGAGACTTCATTTTATT 758

070 CACCATTCTCCAGGCAGTTACAGATGTGATTCGTATCAACGGGGCGTGATGTGTCCTGGC 938

750 CACCTTCCTCCACGCTTACAGATGTGATTCGTATCAACGGCGGTGATGTTGCTCCCTGGC 818

010 AACCAATACAGCATCCGGTCTGCGCTATGACATGCT 998

||||| 878

105

[illegible]

111

[illegible]

ДВ 117

[illegible][illegible]

QY 119 GATGACCCCGCTCAAGGAAGGGCAGTGTGCCCTCATGTTGTCGTTTG

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Db 1059 GACGACCCGCTCATGATGAGGCGAGTGCCTCCATCTTCAACAGGCCATGGTTCCTGAG 1118
 QY 1239 AACATGGGATATACCGCTTACCAAAATGSCATGAGACAGGTGCGGGCCATATCA 1298
 Db 1119 AACAAATGGGATACCGCTTACCAAAATGSCATGAGACAGGTGCGGGCCATATCA 1178
 QY 1299 GATACACATGTGTGTTTCTGAGATCAGAGAGGAAATCATCTTGAAGTTTGGCCAG 1358
 Db 1179 GAATACACATGTGTGTTTCTGAGATCAGAGAGGAAATCATCTTGAAGTTTGGCCAG 1238
 QY 1359 AATGAGAAATAGTGTGTTTCTTAATGACAGCTTTTCCGAGAGATGAGTGTATACA 1418
 Db 1239 AATGAGAAATAGTGTGTTTCTTAATGACAGCTTTTCCGAGAGATGAGTGTATACA 1298
 QY 1419 CTTGTAATAATGATGATGATGAGTGAAGTGAACAAAAGATCATGAGGATCAGATGGA 1478
 Db 1299 CTTGTAATAATGATGATGATGAGTGAAGTGAACAAAAGATCATGAGGATCAGATGGA 1358
 QY 1479 CAGAGCAAGCAGCTCTGTATGTTGCGTTCTCACTGTGTGATTAAGTTGCCCTTGG 1538
 Db 1359 CAGAGCAAGCAGCTCTGTATGTTGCGTTCTCACTGTGTGATTAAGTTGCCCTTGG 1418
 QY 1539 CCGGTGTGACACATGAGGAAAGTGTAAAAAACCCTGTATGCTCCAGAGACCATATGG 1598
 Db 1419 CCGGTGTGACACATGAGGAAAGTGTAAAAAACCCTGTATGCTCCAGAGACCATATGG 1478
 QY 1599 TGGATGATTAAGAGAGTGTGCTGACGACCATTTATCACCACACAGAG-----ACTG 1653
 Db 1479 TGGATGATTAAGAGAGTGTGCTGACGACCATTTATCACCACACAGAGAGAGAG 1538
 QY 1479 TGGATGATTAAGAGAGTGTGCTGACGACCATTTATCACCACACAGAGAGAGAG 1538
 Db 1539 AGGCTTGTGTTGCTTGTGATGTCACGGGTTCACCTTACACAGATGCTTATATCACTTC 1598
 QY 1654 ACTTTTGACAGGACATAGAGCGTGGCAATACAGATGTTGAGGAGACTGTCCAAATGCC 1713
 Db 1539 AGGCTTGTGTTGCTTGTGATGTCACGGGTTCACCTTACACAGATGCTTATATCACTTC 1598
 QY 1714 TTGTGCGACTGATGAGGCTTCCATGCTTCCCTCCAGCACAACACATCAGATGAG 1773
 Db 1599 ACTATGAGACACACATCCATCATATCAGACAGCTCAGAAAGGGCCGCTCAGTGA 1658
 QY 1774 ACGGCTCAGAGGGGATGAG----- 1794
 Db 1659 AGGGGGTGAAGGGGAAAGTGCACACTTAACCATTTTCAGTTAGTTACTGTTGCTGT 1718
 QY 1795 -----TCTAGGGGAGGAATGCTGACTGGAAAGCTTGTCTGA 1832
 Db 1719 GTCTTACAGCTTAGGGTGTGTAATGGGGTGGGTTGCTTAAAGGCAAAACATTTTCCC 1778
 QY 1833 CTACACTGACAGACAGACCTTTGGGGGCAAGTGTCTCCCATATATCACCACAAAGAA 1892
 Db 1779 CAGACGAGAGCTCCGTTGGCCACAAAGGGGTCTGTGGAAAAAATCCCACTGGAAAGCCA 1838
 QY 1893 GGGAGATATCGGGAAAGTTACCTCAAAAGGSCACAGACAGCTGGTCCGTCACCCCTTT 1952
 Db 1839 GAGAGTATTCGGGAAAGTTACCTCAAAAGGSCACAGACAGCTGGTCCGTCACCCCTTT 1898
 QY 1953 GGGCATTCAGTATCTGCTTTCGTCATGGGGGCGCTTCTCCGGGCAATCACCGTCTA 2012
 Db 1899 GGGCATTCAGTATCTGCTTTCGTCATGGGGGCGCTTCTCCGGGCAATCACCGTCTA 1958
 QY 2013 CTGCGTGTGATCATGAGGGGCAAAAGCCTGGTGTGTCAGAGGCAAGGAGAGAGCT 2072
 Db 1959 CTGCGTGTGATCATGAGGGGCAAAAGCCTGGTGTGTCAGAGGCAAGGAGAGAGCT 2018
 QY 2073 CACCACTCGCGCGGGGCTTCATGAGCAGCGTACCAAGCTCAGCGGCTCTTTGGGGA 2132
 Db 2019 CACCACTCGCGCGGGGCTTCATGAGCAGCGTACCAAGCTCAGCGGCTCTTTGGGGA 2078
 QY 2133 CACTCAATCCAAAGACCCAAAGCCGGAGGCTATCTCAAGCCTCATATGCAAAAGGCAA 2192
 Db 2079 CACTCAATCCAAAGACCCAAAGCCGGAGGCTATCTCAAGCCTCATATGCAAAAGGCAA 2138
 QY 2193 GCTGGCAGCTCCGGGCAACAGGGCAGATGCTCATTAAGACACAGCAGCAGCAGCTGGA 2252
 Db 2139 GCTGGCAGCTCCGGGCAACAGGGCAGATGCTCATTAAGACACAGCAGCAGCAGCTGGA 2198

QY 2253 CTTGACGGGCTCTCCCAACCCAGAGTCAACCCCAAGCTGCAAGAGAAAGGAGCCAG 2312
 Db 2199 CTTGACGGGCTCTCCCAACCCAGAGTCAACCCCAAGCTGCAAGAGAAAGGAGCCAG 2258
 QY 2313 CCGGGGACCGCGAGTGGAGAGACACAGACTCATTAATGCTTCCGACAAAGAGACT 2372
 Db 2259 CCGGGGACCGCGAGTGGAGAGACACAGACTCATTAATGCTTCCGACAAAGAGACT 2318
 QY 2373 GCCCCCATGGGCTCCCTGTGATTCGCCAGGACCTGCCCCCTGCGGGGCTCCCGACGCA 2432
 Db 2319 GCCCCCATGGGCTCCCTGTGATTCGCCAGGACCTGCCCCCTGCGGGGCTCCCGACGCA 2378
 QY 2433 CATCCCAAGCTGTGTTCTCTCCATCAGCAGAGGCTTACAGCATGATGATGATGGA 2492
 Db 2379 CATCCCAAGCTGTGTTCTCTCCATCAGCAGAGGCTTACAGCATGATGATGATGGA 2438
 QY 2493 CCAGCCCAAAATGAGAGAGTGGCCAGATGGCGGTGGAGAGCAGAGCCGCAACTGGA 2552
 Db 2439 CCAGCCCAAAATGAGAGAGTGGCCAGATGGCGGTGGAGAGCAGAGCCGCAACTGGA 2498
 QY 2553 GTATAAGACCATCAAGAAATCTCAGCAGAAAGTCCCAACCATGGGGTGAACCTGT 2612
 Db 2499 GTATAAGACCATCAAGAAATCTCAGCAGAAAGTCCCAACCATGGGGTGAACCTGT 2558
 QY 2613 GGAAGAACTGGACAGCTGCCCCCAAAAGTTCACAGCGGGAGAGCTTCCCTGGGTCCCC 2672
 Db 2559 GGAAGAACTGGACAGCTGCCCCCAAAAGTTCACAGCGGGAGAGCTTCCCTGGGTCCCC 2618
 QY 2673 GGAAGCTCCCTGTCTCAAGCGGGTCTAAGCAAGCGGCTGGAATGACACTCTCTTC 2732
 Db 2619 GGAAGCTCCCTGTCTCAAGCGGGTCTAAGCAAGCGGCTGGAATGACACTCTCTTC 2678
 QY 2733 CTACGGGGTGTACTATAGAGAGTACCCACAGAACTGCTCAGAGAAAGCAACAGGC 2792
 Db 2679 CTACGGGGTGTACTATAGAGAGTACCCACAGAACTGCTCAGAGAAAGCAACAGGC 2738
 QY 2793 CACCACTCTCAAAAGAAACAACTACTCTCTCTCAATCTCTCACCTCTCCAGAAACCA 2852
 Db 2739 CACCACTCTCAAAAGAAACAACTACTCTCTCTCAATCTCTCACCTCTCCAGAAACCA 2798
 QY 2853 GAGCTTTGGGAGGAGACAAACCGCGCGCCGCGCCGAGAGGGTGGACTCCATCCAGT 2912
 Db 2799 GAGCTTTGGGAGGAGAGACAAACCGCGCGCCGCGCCGAGAGGGTGGACTCCATCCAGT 2858
 QY 2913 GCAAGCTCCCAAGCATCTGGCCAGGCGGTGACTGTCTGAGAGGACGCCCTCAACGC 2972
 Db 2859 GCAAGCTCCCAAGCATCTGGCCAGGCGGTGACTGTCTGAGAGGACGCCCTCAACGC 2918
 QY 2973 CTACACTCTCAGCAAGGTCGCGGCTGGAAGCGTACGCGCTGTAAGCGGAGCTTAC 3032
 Db 2919 CTACACTCTCAGCAAGGTCGCGGCTGGAAGCGTACGCGCTGTAAGCGGAGCTTAC 2978
 QY 3033 CCCCACCAATCTCTTCTCTCCCTTCCATCCTCATGAAGCCCAATGATGCTGTACATA 3092
 Db 2979 CCCCACCAATCTCTTCTCTCCCTTCCATCCTCATGAAGCCCAATGATGCTGTACATA 3038
 QY 3093 A 3093
 Db 3039 A 3039

RESULT 9
 AAS89721.
 ID AAS89721 standard; cDNA; 3039 BP.
 XX
 AC AAS89721:
 XX
 XX 13-FEB-2002 (first entry)
 DF
 XX
 DB DNA encoding novel human diagnostic protein #25525.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;


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QY 1833 CTCACCTGACAGACAGACCTTTGGGGGAGTGTCTTCCATTAATCACCAGACAGAA 1892
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Db 1779 CAGAGGGAGGCTCCGGTGGCCACAAAGGGGTGTGGAAAAGATCCCAACTGGAAAGCCA 1838
QY 1893 GGGAGTGAATCGGGAAAGTTACTCTAAAGGCCACGACAGCTGTTCCTCCGTAACCTCTT 1952
    |||
Db 1839 GAGATGATTCGGGAAAGTTACTCTAAAGGCCACGACAGCTGTTCCTCCGTAACCTCTT 1898
QY 1953 GGGCATTTGAGTCAATCCTGGCTTGTCTAATGGGGGGCGTCTCTCTGGGATCAGCTCTA 2012
    |||
Db 1899 GGGCATTTGAGTCAATCCTGGCTTGTCTAATGGGGGGCGTCTCTCTGGGATCAGCTCTA 1958
QY 2013 CTGCTGTGTGATCATCGGCGCAAAAGCTGTGCTGTGTGTCAGCGCAGAGAGAGAGCT 2072
    |||
Db 1959 CTGCTGTGTGATCATCGGCGCAAAAGCTGTGCTGTGTGTCAGCGCAGAGAGAGAGCT 2018
QY 2073 CACCCACTCGCGCGGGGCTCCATGAGCAGCGCTCACCAAGCTCAGCGGCTCTTTGGGGA 2132
    |||
Db 2019 CACCCACTCGCGCGGGGCTCCATGAGCAGCGCTCACCAAGCTCAGCGGCTCTTTGGGGA 2078
QY 2133 CACTCAATCCAAAGACCCAAAGCGGAGGCTCTCAGCGCTCATGATGACAAAGGCA 2192
    |||
Db 2079 CACTCAATCCAAAGACCCAAAGCGGAGGCTCTCAGCGCTCATGATGACAAAGGCA 2138
QY 2193 GCTCGGCACTCCGCGCAGACAGGCTCATTAAGACAGACAGCAGCAGCTTGA 2252
    |||
Db 2139 GCTCGGCACTCCGCGCAGACAGGCTCATTAAGACAGACAGCAGCAGCTTGA 2198
QY 2253 CCTGAGCGGCGCTCCCAACCCAGAGTCAACCCAGCGCTCAGCAGAGAGAGAGAGCT 2312
    |||
Db 2199 CCTGAGCGGCGCTCCCAACCCAGAGTCAACCCAGCGCTCAGCAGAGAGAGAGAGCT 2258
QY 2313 CCGCGGAGAGCGGAGTGGGAGAGAACTCATTAAGCTCATTAAGCTCATTAAGAGCAT 2372
    |||
Db 2259 CCGCGGAGAGCGGAGTGGGAGAGAACTCATTAAGCTCATTAAGCTCATTAAGAGCAT 2318
QY 2373 GCCGCCCATGGGCTCCCTGTGATTTCCACAGGAGCTTCCCTGGGGGCTCCCCAGCA 2432
    |||
Db 2319 GCCGCCCATGGGCTCCCTGTGATTTCCACAGGAGCTTCCCTGGGGGCTCCCCAGCA 2378
QY 2433 CATCCCAAGCGTGTGTCTCTGCTCCATCAGCAGCAGGCTTACAGAGATAGTATGCTGA 2492
    |||
Db 2379 CATCCCAAGCGTGTGTCTCTGCTCCATCAGCAGCAGGCTTACAGAGATAGTATGCTGA 2438
QY 2493 CCAGCCCAAAATGAGCGAGTGGCCAGATGGGCTGAGAGACCGGCGCACACTGGA 2552
    |||
Db 2439 CCAGCCCAAAATGAGCGAGTGGGCGCAGATGGGCTGAGAGACCGGCGCACACTGGA 2498
QY 2553 GTATTAAGACCATCAAGAGACATCTCAGCAGCAGAGTCCCAACCATGGGGTGAACCTTGT 2612
    |||
Db 2499 GTATTAAGACCATCAAGAGACATCTCAGCAGCAGAGTCCCAACCATGGGGTGAACCTTGT 2558
QY 2613 GGAAGACCTGAGACGCTGCCCCCAAGTTCACAGGGGAGGCGTCCCTGGGGCCCCC 2672
    |||
Db 2559 GGAAGACCTGAGACGCTGCCCCCAAGTTCACAGGGGAGGCGTCCCTGGGGCCCCC 2618
QY 2673 GGGAGCGCTCCCTGTCTCAGACCGGCTCTAAGCAAGGCTGGAATGACCACTCCTTTC 2732
    |||
Db 2619 GGGAGCGCTCCCTGTCTCAGACCGGCTCTAAGCAAGGCTGGAATGACCACTCCTTTC 2678
QY 2733 CTAGGGGTTGACTATAAGAGAGTACCCCAAGACTGCTCAGAGAGACCCAGG 2792
    |||
Db 2679 CTAGGGGTTGACTATAAGAGAGTACCCCAAGACTGCTCAGAGAGACCCAGG 2738
QY 2793 CACCACTCTCAAAAGAAACACACACTCTCTCAATCTCTCTCTCAGAAACCA 2852
    |||
Db 2739 CACCACTCTCAAAAGAAACACACACTCTCTCTCAATCTCTCTCTCAGAAACCA 2798
QY 2853 GAGCTTTGGAGAGGAGAAACCCGCGCGCGCGCGAGAGAGGTGAGCTCCATCAGGT 2912
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Db 2799 GAGCTTTGGAGAGGAGAAACCCGCGCGCGCGCGAGAGAGGTGAGCTCCATCAGGT 2858

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QY 2913 GCACAGCTCCAGCCATCGGCGAGGCGGTGACTGTCTGAGAGACCCAGCTCAACGC 2972
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Db 2859 GCACAGCTCCAGCCATCTGGCCAGGCGCTGACTGTCTGAGAGACCCAGCTCAACGC 2918
QY 2973 CTACAACTCTACGACAAAGGTGCGGGGTGAAGCGTACGCCCTGCTAAAGCGGAGCTACC 3032
    |||
Db 2919 CTACAACTCTACGACAAAGGTGCGGGGTGAAGCGTACGCCCTGCTAAAGCGGAGCTACC 2978
QY 3033 CCCCAGCAATCTCTTGTCTCCCTTTCCACATCTCAGAGGCCCAATGATGCGGTACATA 3092
    |||
Db 2979 CCCCAGCAATCTCTTGTCTCCCTTTCCACATCTCAGAGGCCCAATGATGCGGTACATA 3038
QY 3093 A 3093
    |||
Db 3039 A 3039

```

RESULT 10

AAH17625
ID AAH17625 standard; cDNA; 3041 BP.

AC AAH17625;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:17153.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PE 28-JUL-2000; 2000EP-0116126.

PF 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

PR (HELI-) HELIX RES INST.

PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

PT primer sets for synthesizing polynucleotides, particularly the 5602.

PT full-length cDNAs defined in the specification, and for the detection

PT full-length cDNAs -

PS Claim 8; SEQ ID 17153; 2537BP + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification, where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a 3'-end sequence, where the

CC polynucleotide which comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 1041 BP; 804 A; 886 C; 714 G; 637 T; 0 other;

Query Match 70.6%; Score 2182.4; DB 22; Length 3041;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2183; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 910 CSTATCAACGGGCGCTGATGTGTCTGCGAAGCTTTTCTACACCTTATACAGATCCCT 969
 DB 1 CSTATCAACGGGCGCTGATGTGTCTGCGAAGCTTTTCTACACCTTATACAGATCCCT 60
 QY 970 GGGTGTGACGTCTGTGCTTATGACATGCTTGAACATTTGCCAGTGTTTTACTGGAGATTC 1029
 DB 61 GGGTGTGACGTCTGTGCTTATGACATGCTTGAACATTTGCCAGTGTTTTACTGGAGATTC 120
 QY 1030 AAGGAACAGAGTCTGCTGATTCACCTGAGACACCGTTCCTGATGAAGAGTTCCTAG 1089
 DB 121 AAGGAACAGAGTCTGCTGATTCACCTGAGACACCGTTCCTGATGAAGAGTTCCTAG 180
 QY 1090 CCCAGGCGAGGTGTGCTGCTGCTCATCTCCCTTAGAAAGATATGCAACCTCCATGAG 1149
 DB 181 CCCAGGCGAGGTGTGCTGCTGCTCATCTCCCTTAGAAAGATATGCAACCTCCATGAG 240
 QY 1150 TTCCCTGATGATACCTGTAACCTTCAATCAAGACGACACCCTCTATGATAGAGATGCC 1209
 DB 241 TTCCCTGATGATACCTGTAACCTTCAATCAAGACGACACCCTCTATGATAGAGATGCC 300
 QY 1210 TTCCATCTAACAGGCGATGGTCTCTGAGACAAATGTCAGATACCGCTTACCAAAAT 1269
 DB 301 TTCCATCTAACAGGCGATGGTCTCTGAGACAAATGTCAGATACCGCTTACCAAAAT 360
 QY 1270 GCATGGACACACAGCTCTGCGGACATATCAGAAATCAGACTGTGTTTCTGGATCAGAG 1329
 DB 361 GCATGGACACACAGCTCTGCGGACATATCAGAAATCAGACTGTGTTTCTGGATCAGAG 420
 QY 1330 AAGGGAATCATCTTGAAGTTTTTGGCCAGAAATAGAGAAATAGTGGTTTTCTAAATGACAGC 1389
 DB 421 AAGGGAATCATCTTGAAGTTTTTGGCCAGAAATAGAGAAATAGTGGTTTTCTAAATGACAGC 480
 QY 1390 CTTTCTGAGAGAGATGAGTGTCTTAACTGAAATGACAGTATGATGAGAGTCGA 1449
 DB 481 CTTTCTGAGAGAGATGAGTGTCTTAACTGAAATGACAGTATGATGAGAGTCGA 540
 QY 1450 GACAAAAGATCATGGGCGATGACGTGGACAGACAGACAGCTCTGTATGTTGGCTTC 1509
 DB 541 GACAAAAGATCATGGGCGATGACGTGGACAGACAGACAGCTCTGTATGTTGGCTTC 600
 QY 1510 TCTACCTGTGTGATTAAGGTTTCCCTTGGCCGCTGTAAGACATGGGAGTGTAAATAA 1569
 DB 601 TCTACCTGTGTGATTAAGGTTTCCCTTGGCCGCTGTAAGACATGGGAGTGTAAATAA 660
 QY 1570 ACGTGTATGCTTCGAGAGACCATATTTGATGATGATAAAGGAAGGTGGTGCCTGAGC 1629
 DB 661 ACGTGTATGCTTCGAGAGACCATATTTGATGATGATAAAGGAAGGTGGTGCCTGAGC 720
 QY 1630 CATTTATCACCAACAGACAGTACTTTTGAAGAGACATAGAGCTGTGCATATACGAT 1689
 DB 721 CATTTATCACCAACAGACAGTACTTTTGAAGAGACATAGAGCTGTGCATATACGAT 780
 QY 1690 GGTCTGGGGAGTGTGCAATTCCTTTTGGCACTGATGGCAATTCAGTTCCTCTTG 1749
 DB 781 GGTCTGGGGAGTGTGCAATTCCTTTTGGCACTGATGGCAATTCAGTTCCTCTTG 840
 QY 1750 CCGAGCAACCAACATAGATGAGAGGCTCAAGAGGGGTATGATGTAGGGGAGGATG 1809
 DB 841 CCGAGCAACCAACATAGATGAGAGGCTCAAGAGGGGTATGATGTAGGGGAGGATG 900

QY 1810 CTGACCTGAGAGCATCTGCTTACTGCTACCTGACAGACAGACACCTTTGGGGGAGTGTCT 1869
 DB 901 CTGACCTGAGAGCATCTGCTTACTGCTACCTGACAGACAGACACCTTTGGGGGAGTGTCT 960
 QY 1870 TCCCATTAATCACCAGACAGAGAGAGTGTGGGAAAGTTACTCTCAAGGCCAGCAGC 1929
 DB 961 TCCCATTAATCACCAGACAGAGAGAGTGTGGGAAAGTTACTCTCAAGGCCAGCAGC 1020
 QY 1930 CAGCTGTCTCCGCTACCCCTCTTGGCCATTTGACATGATCCCTGCTTGTGATGGGGGCC 1989
 DB 1021 CAGCTGTCTCCGCTACCCCTCTTGGCCATTTGACATGATCCCTGCTTGTGATGGGGGCC 1080
 QY 1990 GTCTCTGGGGCATCACCTCTTACTGCTGTGTGATCATGCGGGCAAAACGCTGGTG 2049
 DB 1081 GTCTCTGGGGCATCACCTCTTACTGCTGTGTGATCATGCGGGCAAAACGCTGGTG 1140
 QY 2050 GTGACGCGAAGAGAGAGAGTCAACCCACTCGCGCGGGGCTCTCATGAGCAGCTCAC 2109
 DB 1141 GTGACGCGAAGAGAGAGTCAACCCACTCGCGCGGGGCTCTCATGAGCAGCTCAC 1200
 QY 2110 AAGCTCAGGGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGAGGCTATCTC 2169
 DB 1201 AAGCTCAGGGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGAGGCTATCTC 1260
 QY 2170 AGCCACTATGACAGAGGCAAGCTCGCCACTCGCCGCAACGCGCCAAAGATGCTCAT 2229
 DB 1261 AGCCACTATGACAGAGGCAAGCTCGCCACTCGCCGCAACGCGCCAAAGATGCTCAT 1320
 QY 2230 AAGGACAGCAGCAGCCACTGTGACCTGACGCGCCCTCCCAACCCAGAGTCAACCCCAAG 2289
 DB 1321 AAGGACAGCAGCAGCAGCCACTGTGACCTGACGCGCCCTCCCAACCCAGAGTCAACCCCAAG 1380
 QY 2290 CTGACAGAGAGGCGAAGCCGAGCCGCGGAGCTGAGTGGAGAGAGAACCGAAGCTTC 2349
 DB 1381 CTGACAGAGAGGCGAAGCCGAGCCGCGGAGCTGAGTGGAGAGAGAACCGAAGCTTC 1440
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 DB 1441 ATCAATGCTGCAAAAGAGCATGCGCCCATGGGCTCCCTGATTTCCACAGGAGCTG 1500
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 DB 1501 CCCCTGGGGCTCCCCCAACCCACATCCCAAGGCTGTGTCTCTGCCATCAGCAGCAG 1560
 QY 2470 GGCTACACGATAGTACGTGACAGCCCAAAATGACGAGGTGGCCGATGAGGCTG 2529
 DB 1561 GGCTACACGATAGTACGTGACAGCCCAAAATGACGAGGTGGCCGATGAGGCTG 1620
 QY 2530 GAGGACGAGGCGCCGACACTGGAGTAAAGCAATCAAGAAACATCTCAGCAGCAAGT 2589
 DB 1621 GAGGACGAGGCGCCGACACTGGAGTAAAGCAATCAAGAAACATCTCAGCAGCAAGT 1680
 QY 2590 CCCAACCATGGGGTGAACCTTGTGAGAACCTTGACAGCTGCCCCCAAAAGTTCCAGC 2649
 DB 1681 CCCAACCATGGGGTGAACCTTGTGAGAACCTTGACAGCTGCCCCCAAAAGTTCCAGC 1740
 QY 2650 CGGAGGCTCTCCCTGGGTCCCCCGGAGGCTCTCTGTCTCAGACCGGCTAAAGCAACGG 2709
 DB 1741 CGGAGGCTCTCCCTGGGTCCCCCGGAGGCTCTCTGTCTCAGACCGGCTAAAGCAACGG 1800
 QY 2710 CTGGAATGACACCTCTCTCTCTAGGGGTTGACTATTAAGAGAGCTACCCACAGAC 2769
 DB 1801 CTGGAATGACACCTCTCTCTCTAGGGGTTGACTATTAAGAGAGCTACCCACAGAC 1860
 QY 2770 TCGCTCAGAGAAACCCACAGGCCACACTCTCAAAAGAAACAACTACTCTCTCAAT 2829
 DB 1861 TCGCTCAGAGAAACCCACAGGCCACACTCTCAAAAGAAACAACTACTCTCTCAAT 1920
 QY 2830 TCTCTCACTCTCTCAAAACCAAGCTTTGGCAGGGAGCAACCCGCGCCGCGCCG 2889
 DB 1921 TCTCTCACTCTCTCAAAACCAAGCTTTGGCAGGGAGCAACCCGCGCCGCGCCG 1980
 QY 2890 CAGAGGGTGAACCTCAATCCAGGTGACAGCTCCAGGCCATCTGCGCAGGCGGTGCT 2949


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QY 829 CTGAGAGCGCGCTTGAAGTCTCAGTCTCGAGAGCTCATTTTATTTCAACATCTC 888
    |||||||
Db 781 CTGAGAGCGCGCTTGAAGTCTCAGTCTCGAGAGCTCATTTTATTTCAACATCTC 840
QY 889 CAGGCAAGTTACAGATGTGATTCATCAACGGGCGTGATGTGCTGGCAACGTTTCT 948
    |||||||
Db 841 CAGGCAAGTTACAGATGTGATTCATCAACGGGCGTGATGTGCTGGCAACGTTTCT 900
QY 949 ACACCTTTATACAGCATCCCTGGGCTGCGAGTCTGTGCCATATACATAGCTTGACATTTGCC 1008
    |||||||
Db 901 ACACCTTTATACAGCATCCCTGGGCTGCGAGTCTGTGCCATATACATAGCTTGACATTTGCC 960
QY 1009 AGTGTTTTCTGGGAGATTCAGAGAACAGAGCTTCCTGATTCACCTGGACACCAAGTT 1068
    |||||||
Db 961 AGTGTTTTCTGGGAGATTCAGAGAACAGAGCTTCCTGATTCACCTGGACACCAAGTT 1020
QY 1069 CCGATGATGAACAGATTCCTTAAGCCAGGCCAGGTTGCTGTGCTGCTCCCTCTTAGAA 1128
    |||||||
Db 1021 CCGATGATGAACAGATTCCTTAAGCCAGGCCAGGTTGCTGTGCTGCTCCCTCTTAGAA 1080
QY 1129 AGATATGCAACCTCCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGAGCCACCG 1188
    |||||||
Db 1081 AGATATGCAACCTCCCAATGAGTTCCCTGATGATACCTGAACTTCATCAAGAGCCACCG 1140
QY 1189 CTCATGATGATGAGGAGTGGCCCTCCATCTCAACAGGCCATGTTCCCTGAGAACATGCTC 1248
    |||||||
Db 1141 CTCATGATGATGAGGAGTGGCCCTCCATCTCAACAGGCCATGTTCCCTGAGAACATGCTC 1200
QY 1249 AGATACCGCCTTACCAAAATTTGCAAGTGGACACAGCTCTGGGCCATATCAGATCACACT 1308
    |||||||
Db 1201 AGATACCGCCTTACCAAAATTTGCAAGTGGACACAGCTCTGGGCCATATCAGATCACACT 1260
QY 1309 GTGGTCTTTTCTGGGATCAGAGAGAGGGAATCATCTTGAAGTTTGGCCAGAAATAGGAAT 1368
    |||||||
Db 1261 GTGGTCTTTTCTGGGATCAGAGAGAGGGAATCATCTTGAAGTTTGGCCAGAAATAGGAAT 1320
QY 1369 AGTGTCTTCTAAATGACAGCTTCTCTGGAGGAGATGATGTTCAACTCTGAAAAA 1428
    |||||||
Db 1321 AGTGTCTTCTAAATGACAGCTTCTCTGGAGGAGATGATGTTCAACTCTGAAAAA 1380
QY 1429 TGCAGCTATGATGAGTGCAGAGACAAAAGATCATGGGATCATGCTGGACAGAGCAAGC 1488
    |||||||
Db 1381 TGCAGCTATGATGAGTGCAGAGACAAAAGATCATGGGATCATGCTGGACAGAGCAAGC 1440
QY 1489 AGCTCTCTGATATGTTGCGTCTCTCACTGTGTGATTAAGTTTCCCTGGCCGGTGGAA 1548
    |||||||
Db 1441 AGCTCTCTGATATGTTGCGTCTCTCACTGTGTGATTAAGTTTCCCTGGCCGGTGGAA 1500
QY 1549 CGACATGGGAAGTGTAAAAAAACCTGTATTGCTCTCAGAGAGACCAATTTGGATGATA 1608
    |||||||
Db 1501 CGACATGGGAAGTGTAAAAAAACCTGTATTGCTCTCAGAGAGACCAATTTGGATGATA 1560
QY 1609 AAGGAAGTGTGCTGCTGACGCCATTTATCACCCAAACAGACAGACTGACTTTTGACAGAGAC 1668
    |||||||
Db 1561 AAGGAAGTGTGCTGCTGACGCCATTTATCACCCAAACAGACAGACTGACTTTTGACAGAGAC 1620
QY 1669 ATAGAGCGTGCATATACAGATGATGTGGGGGACGTGCACAAATTCCTTTGGCACTGAT 1728
    |||||||
Db 1621 ATAGAGCGTGCATATACAGATGATGTGGGGGACGTGCACAAATTCCTTTGGCACTGAT 1680
QY 1729 GGGCATTCACATCCCTCTTCCAGACAGCAACACATCATGATTCAGCGCTCAAGAGGGG 1788
    |||||||
Db 1681 GGGCATTCACATCCCTCTTCCAGACAGCAACACATCATGATTCAGCGCTCAAGAGGGG 1740
QY 1789 TATGAGTCTAAGGGAGGAATGCTGAGTGAAGCATCTGCTTGACTCACTGACAGCACA 1848
    |||||||
Db 1741 TATGAGTCTAAGGGAGGAATGCTGAGTGAAGCATCTGCTTGACTCACTGACAGCACA 1800
QY 1849 GACCTTTGGGGGCGAGTCTTCCCATATATCAACCAAGCAAGAGGGAGTGTGGGGA 1908
    |||||||
Db 1801 GACCTTTGGGGGCGAGTCTTCCCATATATCAACCAAGCAAGAGGGAGTGTGGGGA 1860

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QY 1909 AGTTACCTCAAGGCCACGACCACTGG 1936
    |||||||
Db 1861 AGTTACCTCAAGGCCACGACCACTGG 1888

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RESULT 12

AAH15834

ID AAH15834 standard; cDNA; 2293 BP.

XX

AAH15834;

XX

26-JUN-2001 (first entry)

XX

Human cDNA sequence SEQ ID NO:14327.

DE

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

KW

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OS

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Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 other;

Query Match 59.0%; Score 1824.4; DB 22; Length 2293;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1825; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1268	TTGACAGGACACACGCTGGGGCCATACAGATACACACTGGGTGTTTTCJGAGATCAG	1327
Db	1	TTGCAGTGGACACAGCTGCTGGGCCATATACAAATACACTGTGGTTTTTCJGGGATCAG	60
QY	1328	AGAAGGGAAATCATCTTGAAAGTTTTTGGCCAGAAATAGGAAATAGTGGTTTTTCTAAATGACA	1387
Db	61	AGAAGGGAAATCATCTTGAAAGTTTTTGGCCAGAAATAGGAAATAGTGGTTTTTCTAAATGACA	120
QY	1388	GCCCTTTTCCGGAGAGATGAGTGTTTACAACTGTAAAAATGCACCTATAGATGAGACTG	1447
Db	121	GCCCTTTTCCGGAGAGATGAGTGTTTACAACTGTAAAAATGCACCTATAGATGAGACTG	180
QY	1448	AACACAAAAGATCATGGGCATGCACCTGGACAGACAGACACCTCTGTATGTGGCT	1507
Db	181	AACACAAAAGATCATGGGCATGCACCTGGACAGACAGACACCTCTGTATGTGGCT	240
QY	1508	TCTCTACCTGTGTGATTAAGGTTCCCTTGGCCGGTGTGAACACATGGGAAGTGTAAAA	1567
Db	241	TCTCTACCTGTGTGATTAAGGTTCCCTTGGCCGGTGTGAACACATGGGAAGTGTAAAA	300
QY	1568	AAACCTGTATGGCTCCAGAGCCCATATGTGGATGATTAAGGAAGAGGTGGCTGCA	1627
Db	301	AAACCTGTATGGCTCCAGAGCCCATATGTGGATGATTAAGGAAGAGGTGGCTGCA	360
QY	1628	GCCATTTATACCCCAACAGCAGACTGACTTTTGAAGCAGACATAGACGTGGCAATACAG	1687
Db	361	GCCATTTATACCCCAACAGCAGACTGACTTTTGAAGCAGACATAGACGTGGCAATACAG	420
QY	1688	ATGATGTGGGGAGATGTACAAATTCCTTGTGGCAGATGAAATGGACATTCAGTCCCTCT	1747
Db	421	ATGATGTGGGGAGATGTACAAATTCCTTGTGGCAGATGAAATGGACATTCAGTCCCTCT	480
QY	1748	TGCCACAGCACACCCATCAGATTGACGGGCTCAAGAGGGTATGAGTCTTAGGGGAGAA	1807
Db	481	TGCCACAGCACACCCATCAGATTGACGGGCTCAAGAGGGTATGAGTCTTAGGGGAGAA	540
QY	1808	TGCTGGACTGGAAACATCTGCTGACCTGACCTGCACACACAGACCTTTGGGGGCACTGT	1867
Db	541	TGCTGGACTGGAAACATCTGCTGACCTGACCTGCACACACAGACCTTTGGGGGCACTGT	600
QY	1868	CTTCCCATTAATCACCAACAGACAAAGAAAGGAGTGTTCGGGAAAGTTTACCTCAAAAGGCCACG	1927
Db	601	CTTCCCATTAATCACCAACAGACAAAGAAAGGAGTGTTCGGGAAAGTTTACCTCAAAAGGCCACG	660
QY	1928	ACACAGCTGTCCCGTACACCTCTTGGCCATGTGACATCACTCTGGCTTGTGCTATGGGGG	1987
Db	661	ACACAGCTGTCCCGTACACCTCTTGGCCATGTGACATCACTCTGGCTTGTGCTATGGGGG	720
QY	1988	CCGACTCTCGGGGCATCACCCTACTACGCGCTGTGATCATCGCGCAAAAGACCTGGCTG	2047
Db	721	CCGACTCTCGGGGCATCACCCTACTACGCGCTGTGATCATCGCGCAAAAGACCTGGCTG	780
QY	2048	TGCTGCACGCGCAAGAGAGAGCTCAACCACTGCGCGCGGGGCTCCATGACGAGCTCA	2107
Db	781	TGCTGCACGCGCAAGAGAGAGAGCTCAACCACTGCGCGCGGGGCTCCATGACGAGCTCA	840
QY	2108	CCAAGCTCAGGGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAAGGCCATATC	2167
Db	841	CCAAGCTCAGGGGCTCTTTGGGGACACTCAATCCAAAGACCCAAAGCCGGAAGGCCATATC	900
QY	2168	TCACGGCCACTATGCACAAAGCGCAAGCTCGCCACTTCCGGGCACACAGGCCCAAGATGCTCA	2227
Db	901	TCACGGCCACTATGCACAAAGCGCAAGCTCGCCACTTCCGGGCACACAGGCCCAAGATGCTCA	960
QY	2228	TTTAAAGCAGACACGACCACTGGAAGTGAAGGCGCTTCCCAACCCCAAGTCAACCCCAA	2287
Db	961	TTTAAAGCAGACACGACCACTGGAAGTGAAGGCGCTTCCCAACCCCAAGTCAACCCCAA	1020
QY	2288	CGCTGCACACAAAGGGAAGCCACAGCCGCGCAGCGGAGTGTGGGAGAGGAACAGAAAC	2347
Db	1021	CGCTGCACACAAAGGGAAGCCACAGCCGCGCAGCGGAGTGTGGGAGAGGAACAGAAAC	1080

QY	2248	TCATCATTCGCTGACAAAGACACATATGCCCCCAATAGGGGCTCCCTGTAATTCACCAAGGAC	2407
Db	1081	TCATCATTCGCTGACAAAGACACATATGCCCCCAATAGGGGCTCCCTGTAATTCACCAAGGAC	1140
QY	2408	TGCCCCCTGCGGGGCTCCGCCAGGCCACATCCCCAGCGTGThgTgTCTTGCCCATACGACG	2457
Db	1141	TGCCCCCTGCGGGGCTCCGCCAGGCCACATCCCCAGCGTGThgTgTCTTGCCCATACGACG	1200
QY	2468	AGGGCTACACAGATAGTACTGATGGACACAGCCCAAAATAGAGGAGGTGGGCCATGGGCGC	2527
Db	1201	AGGGCTACACAGATAGTACTGATGGACACAGCCCAAAATAGAGGAGGTGGGCCATGGGCGC	1250
QY	2528	TGGAGGACACAGGCGCGCACACTGGAGATATAAGACATCAAGAAATCTCAGACAGCAAGA	2587
Db	1261	TGGAGGACACAGGCGCGCACACTGGAGATATAAGACATCAAGAAATCTCAGACAGCAAGA	1320
QY	2588	GTCGCCAACCATGGGGTGAACCTTTGGAGAACTTGGACAGGCTGCCCCCAAAATGTCAC	2647
Db	1321	GTCGCCAACCATGGGGTGAACCTTTGGAGAACTTGGACAGGCTGCCCCCAAAATGTCAC	1380
QY	2648	AGGGGAGAGGCTCCCTGGGTGCCCCCGGAGGCTCCCTGTCTCAGACCGGTGTAAAGCAAGC	2707
Db	1381	AGGGGAGAGGCTCCCTGGGTGCCCCCGGAGGCTCCCTGTCTCAGACCGGTGTAAAGCAAGC	1440
QY	2708	GGCTGGAATGACCACTCTCTTCTCTACGSGGGTTGACTATATAGAGAGCTTACCCACGA	2767
Db	1441	GGCTGGAATGACCACTCTCTTCTCTACGSGGGTTGACTATATAGAGAGCTTACCCACGA	1500
QY	2768	ACTGCGTACAGAGAAAGCACCAGGCGCACACTCTCTCAAAAGAAAGAACACTTAACCTTCCA	2827
Db	1501	ACTGCGTACAGAGAAAGCACCAGGCGCACACTCTCTCAAAAGAAAGAACACTTAACCTTCCA	1560
QY	2828	ATTCCTCTACACTCTCTCCAGAAACCAAGAGCTTTGGGAGGGGAGACACCCGCGCGCGCC	2887
Db	1561	ATTCCTCTACACTCTCTCCAGAAACCAAGAGCTTTGGGAGGGGAGACACCCGCGCGCGCC	1620
QY	2888	CGCAGAGGGTGGACTCCATCCAGGTGACAGCTCCACGCACTTGTGGCGAGCGCTGACTG	2947
Db	1621	CGCAGAGGGTGGACTCCATCCAGGTGACAGCTCCACGCACTTGTGGCGAGCGCTGACTG	1680
QY	2948	TCTCGAGGACAGCCAGCCTCAAGGCTTACAACTCACTGACAAAGGTGCGGGGCTGAAGCGTA	3007
Db	1681	TCTCGAGGACAGCCAGCCTCAAGGCTTACAACTCACTGACAAAGGTGCGGGGCTGAAGCGTA	1740
QY	3008	CGCCCTCGCTAAAGCGGAGCGTACCCGCCAAACGATCTCTTGTCCCTTTCCACATCCA	3067
Db	1741	CGCCCTCGCTAAAGCGGAGCGTACCCGCCAAACGATCTCTTGTCCCTTTCCACATCCA	1800
QY	3068	TGAAGCCCAATGATGCTGTACATTA 3093	
Db	1801	TGAAGCCCAATGATGCTGTACATTA 1826	
RESULT 13			
XX	AAK94365	AAK94365 standard; cDNA; 2227 BP.	
XX	AAK94365;		
AC	06-NOV-2001	(first entry)	
XX	06-NOV-2001	(first entry)	
DT	Human full-length cDNA, SEQ ID NO: 3087.		
XX	Human full-length cDNA; cDNA synthesis; oligo-capping; ss.		
DE	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
XX	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
KW	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
XX	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
OS	Homo sapiens.		
XX	Homo sapiens.		
PN	EP1130094-A2.		
XX	EP1130094-A2.		
PD	05-SEP-2001.		
XX	05-SEP-2001.		
PF	07-JUL-2000; 2000EP-0114089.		
XX	07-JUL-2000; 2000EP-0114089.		

PR 08-JUL-1999: 99JP-0194486-
 PR 11-JAN-2000: 2000JP-0118774.
 PR 02-MAY-2000: 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX WPI: 2001-524255/58.
 DR F-PSDB: AAM93444.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 XX Claim 8: SEQ ID NO 3087; 1380bp + sequence listing; English.
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesized by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a full length
 CC human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX
 SQ Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 other;
 Query Match 56.38; Score 1742.4; DB 22; Length 2227;
 Best local Similarity 99.9%; Pred. No. 0;
 Matches 1743; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1350 TTGGCCAGAAATGGAATAGTGTGTTTCTTAATGACAGCCTTTCTCGAGAGATGAG 1409
 DB 1 TTGGCCAGAAATGGAATAGTGTGTTTCTTAATGACAGCCTTTCTCGAGAGATGAG 60
 QY 1410 TGTTCACACTCTGAAAAATGACGATATGATGAGTGGAGACAAAAGATCATGGCAT 1469
 DB 61 TGTTCACACTCTGAAAAATGACGATATGATGAGTGGAGACAAAAGATCATGGCAT 120
 QY 1470 GCAGCTGACAGACAGACAGCCTCTGTATGTTGGCTCTCTACCTGTGATTAAGT 1529
 DB 121 GCAGCTGACAGACAGACAGCCTCTGTATGTTGGCTCTCTACCTGTGATTAAGT 180
 QY 1530 TCCCTTGCGCGGTGTGACAGCATGGAAGTGTAAAAAAACCTGTATTGCTTCCAGAGA 1589
 DB 181 TCCCTTGCGCGGTGTGACAGCATGGAAGTGTAAAAAAACCTGTATTGCTTCCAGAGA 240
 QY 1590 CCCATATTGATGATTAAGGAAGTGTGCTGACAGCATTTATACCCACAGAGAG 1649
 DB 241 CCCATATTGATGATTAAGGAAGTGTGCTGACAGCATTTATACCCACAGAGAG 300
 QY 1650 ACTGACTTTGAGAGAGCATAGAGCGTGGCATATAGATGTCTGGGGAGCTGTCAAA 1709
 DB 301 ACTGACTTTGAGAGAGCATAGAGCGTGGCATATAGATGTCTGGGGAGCTGTCAAA 360
 QY 1710 TTCTTTGTGACACTGATGGCATTTCCATTCCTCTTGGCCACAGACACACATCAGA 1769
 DB 361 TTCTTTGTGACACTGATGGCATTTCCATTCCTCTTGGCCACAGACACACATCAGA 420
 QY 1770 TTGACAGGCTCAAGAGGGGTATGATCTAGGGGAGGAATGCTGAGCTGGAAAGCATCTGCT 1829
 DB 421 TTGACAGGCTCAAGAGGGGTATGATCTAGGGGAGGAATGCTGAGCTGGAAAGCATCTGCT 480
 QY 1830 TGACTCAGCTAGACAGACAGACCCCTTTGGGGAGAGTGTCTCCCAATATCACAAGACAA 1889
 DB 481 TGACTCAGCTAGACAGACAGACCCCTTTGGGGAGAGTGTCTCCCAATATCACAAGACAA 540
 QY 1890 GAAGGAGTGAATTCGGGAAGTTACCTCAAAAGGCCAGACAGCTGTGTTCCGTCACCT 1949

DB 541 GAAGGAGTGAATTCGGGAAGTTACCTCAAAAGGCCAGACAGCTGTGTTCCCTACCT 600
 QY 1950 CTTGGCCATTGCGAGTATCATCTGCTTCTCATGAGGGGCGCTTTCTCGGGCATCAACCT 2009
 DB 601 CTTGGCCATTGCGAGTATCATCTGCTTCTCATGAGGGGCGCTTTCTCGGGCATCAACCT 660
 QY 2010 CTACTGCGTCTGTGATCATGCGGCAAGACGTGCTGTGTGTGACGCGCAAGAGAAAGA 2069
 DB 661 CTACTGCGTCTGTGATCATGCGGCAAGACGTGCTGTGTGTGACGCGCAAGAGAAAGA 720
 QY 2070 GCTCACCACACTGCGCGGGGCTCCATGAGACCGTCCACAGCTCAGAGGCGCTTTGG 2129
 DB 721 GCTCACCACACTGCGCGGGGCTCCATGAGACCGTCCACAGCTCAGAGGCGCTTTGG 780
 QY 2130 GGCACTCATATCCAAAGACCCAAAGCGGAGGCGCATCTCTACGCCACTATGACAAACGG 2189
 DB 781 GGCACTCATATCCAAAGACCCAAAGCGGAGGCGCATCTCTACGCCACTATGACAAACGG 840
 QY 2190 CAAGCTCGCCTCTCCGCGCAACAGCGCCAAAGATGCTCATTAAGCAGACCAACCACT 2249
 DB 841 CAAGCTCGCCTCTCCGCGCAACAGCGCCAAAGATGCTCATTAAGCAGACCAACCACT 900
 QY 2250 GGAAGCTGAGCGGCTCTCCACCCAGAGTAAACCCCAAGCGCTGAGCAGAAAGGAGGCC 2309
 DB 901 GGAAGCTGAGCGGCTCTCCACCCAGAGTAAACCCCAAGCGCTGAGCAGAAAGGAGGCC 960
 QY 2310 CAGCGCGGAGCGCGGAGTGGAGAGAGAACCCAACTCATCTCTGACAAAGGA 2369
 DB 961 CAGCGCGGAGCGCGGAGTGGAGAGAGAACCCAACTCATCTCTGACAAAGGA 1020
 QY 2370 CATGCCCCCATGAGGCTCCCTGTGATTCGACAGGACTGCCCTGGGGGCTCTCCAG 2429
 DB 1021 CATGCCCCCATGAGGCTCCCTGTGATTCGACAGGACTGCCCTGGGGGCTCTCCAG 1080
 QY 2430 CCACATCCCAAGCGTGTGTGTCGTCATCAGCAGACAGAGGCTACCAAGCATGAGTACGT 2489
 DB 1081 CCACATCCCAAGCGTGTGTGTCGTCATCAGCAGACAGAGGCTACCAAGCATGAGTACGT 1140
 QY 2490 GGAACAGCCCAAAATGAGCGAGTGTGCGCAGATGGCGCTGAGAGACAGGCGCCCACT 2549
 DB 1141 GGAACAGCCCAAAATGAGCGAGTGTGCGCAGATGGCGCTGAGAGACAGGCGCCCACT 1200
 QY 2550 GGAATATTAAGACCTCAAGGAACATCTCAGAGAGAGTGTCCAAACCATGAGGATGAACT 2609
 DB 1201 GGAATATTAAGACCTCAAGGAACATCTCAGAGAGAGTGTCCAAACCATGAGGATGAACT 1260
 QY 2610 TGTGAGAACCTTGAGACAGCTGCCCCCAAAAGTTCACAGCGGAGAGGCTCTCGGTCC 2669
 DB 1261 TGTGAGAACCTTGAGACAGCTGCCCCCAAAAGTTCACAGCGGAGAGGCTCTCGGTCC 1320
 QY 2670 CCGGGAGGCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGTGGAAATGACCACTCTCTC 2729
 DB 1321 CCGGGAGGCTCCCTGTCTCAGACCGGTCTAAGCAAGCGGTGGAAATGACCACTCTCTC 1380
 QY 2730 TTCTAGGGGTTGCTCTAAGAGAGGTATACCCACGAACCTGCTCAGAGAAAGCACCA 2789
 DB 1381 TTCTAGGGGTTGCTCTAAGAGAGGTATACCCACGAACCTGCTCAGAGAAAGCACCA 1440
 QY 2790 GGCCACACTCTCAAAAGAAACACACTAATCTCTCAATTCCTCTCACTCTCTCAAGAA 2849
 DB 1441 GGCCACACTCTCAAAAGAAACACACTAATCTCTCAATTCCTCTCACTCTCTCAAGAA 1500
 QY 2850 CCAGAGCTTTGGCAGGGAGAGACACCCGCGCGCGCCCGCAGAGAGGTGAGACTCCATCA 2909
 DB 1501 CCAGAGCTTTGGCAGGGAGAGACACCCGCGCGCGCCCGCAGAGAGGTGAGACTCCATCA 1560
 QY 2910 GGTGACAGCTCCCGACCATCTGGCAGAGCGCTGACTGTCTGAGAGCAGCCAGGCTCAA 2969
 DB 1561 GGTGACAGCTCCCGACCATCTGGCAGAGCGCTGACTGTCTGAGAGCAGCCAGGCTCAA 1620
 QY 2970 GGCCTACAACTCACTAGACAAAGTGGGGGTGAAGCTGAGGCTGCTTAAAGCGGAGCT 3029

Db	1126	TTCCCTGTGATTTCOCANCGACACTGCCCTCGGGGCTCTCCGCCAGCCACTATCCCAAGGTG	1185
QY	2446	GTGGTCTCTGCCCATCTACGCAAGAGGGCTACCAAGCATGATGCTGGACACAGCCAAATG	2505
Db	1186	GTGTCTCTGCCCATCTACGCAAGAGGGCTACCAAGCATGATGCTGGACACAGCCAAATG	1245
QY	2506	AGCGAGGTGGCCCCGATGGGGCTGGAGGACAGGGCCGCCACACTAGGATGTAAGACATC	2565
Db	1246	AGCGAGGTGGCCCCGATGGGGCTGGAGGACAGGGCCGCCACACTAGGATGTAAGACATC	1305
QY	2566	AAGGACATCTCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTTGGAGAACCTGAGC	2625
Db	1306	AAGGACATCTCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTTGGAGAACCTGAGC	1365
QY	2626	AGCCTGCCCCCCTCAAGTTTCCACAGCGGGAGGGCTCCCTGGGGTCCCCGGGAGCCTCCCTG	2685
Db	1366	AGCCTGCCCCCCTCAAGTTTCCACAGCGGGAGGGCTCCCTGGGGTCCCCGGGAGCCTCCCTG	1425
QY	2686	TCTTCAGACCGGTCCTACGCAAGCGGGCTGGAATGCAACACTCTCTTCTCTACGGGGTTGAC	2745
Db	1426	TCTTCAGACCGGTCCTACGCAAGCGGGCTGGAATGCAACACTCTCTTCTCTACGGGGTTGAC	1485
QY	2746	TATTAAGAGAGCTACCCCAAGCACTCGCTCAACGAAAGCCACAGGCTCACACTCTCAA	2805
Db	1486	TATTAAGAGAGAGCTACCCCAAGCACTCGCTCAACGAAAGCCACAGGCTCACACTCTCAA	1545
QY	2806	AGAAACAACAATACTCTCTCAATTCCTCTCTACCTCTCCAGAAACCAAGAGCTTTGGCAGG	2865
Db	1546	AGAAACAACAATACTCTCTCAATTCCTCTCTACCTCTCCAGAAACCAAGAGCTTTGGCAGG	1605
QY	2866	GGAGACAAACCCCGCCGCCGCCGAGAGGGTGAATCTCATCTCAAGAGTGCACAGCTCCAG	2925
Db	1606	GGAGACAAACCCCGCCGCCGCCGAGAGGGTGAATCTCATCTCAAGAGTGCACAGCTCCAG	1665
QY	2926	CCATCTGCGCCAGGCGCGTGAATGTCTCGAGGAGGCCCAAGCCTCAAGGCTTACACTGACTG	2985
Db	1666	CCATCTGCGCCAGGCGCGTGAATGTCTCGAGGAGGCCCAAGCCTCAAGGCTTACACTGACTG	1725
QY	3046	TTTGCTCCCTTTCCACATCCATGGAAGCCCAATGATGGGTACATAA 3093	
Db	1786	TTTGCTCCCTTTCCACATCCATGGAAGCCCAATGATGGGTACATAA 1833	
RESULT 15			
ID	AA568253	standard; cDNA; 2592 BP.	
AC	AA568253;		
XX	13-FEB-2002 (first entry)		
DE	DNA encoding novel human diagnostic protein #4057.		
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
OS	Homo sapiens.		
XX	WO200175067-A2.		
XX	11-OCT-2001.		
XX	30-MAR-2001; 2001WO-0S08631.		
XX	31-MAR-2000; 2000US-0540217.		
PR	23-AUG-2000; 2000US-0649167.		
XX	(HYSE-) HYSEQ INC.		
XX			

XX	Dymanac RT, Liu C, Tang YT.
XX	WIPI: 2001-639362/73.
DR	P-P-SDB; ABG04066.
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	Claim 1; SEQ ID No 4057; 103pp; English.
PS	
XX	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
SQ	
XX	Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 other;
Query Match	51.5%; Score 1592; DB 23; Length 2592;
Best Local Similarity	84.3%; Pred. No. 0;
Matches 1809; Conservative	0; Mismatches 325; Indels 12; Gaps 1;
QY	960 CAGCATCCTCGTGGTCGTGCAGTCTGTGCCATATGACATCTTGACATTTGCCAGTCTTTTAC 1019
DB	
447 CAGCATCCTCGTGGTCGTGCAGTCTGTGCCATATGACATCTTGACATTTGCCAGTCTTTTAC 506	
QY	1020 TGGGAGATTCAAGAACAGAAGTCTCCTGATTCACCTGGACACCAGTCTCATGAAGC 1079
DB	
507 TGGGAGATTCAAGAACAGAAGTCTCCTGATTCACCTGGACACCAGTCTCATGAAGC 566	
QY	1080 AGTTCCTAAGCCCAGGCCAGGCTGTCTGTCTGCTGCTACTCTTAGAAAGATATGCAAC 1139
DB	
567 AGTTCCTAAGCCCAGGCCAGGCTGTCTGCTGCTGCTACTCTTAGAAAGATATGCAAC 626	
QY	1140 CTCACATAGTTCCTTGATGATATACCCTGAATTCATAPAAAGCACCCGCTCATAGATGA 1199
DB	
627 CTCACATAGTTCCTTGATGATATACCCTGAATTCATAPAAAGCACCCGCTCATAGATGA 686	
QY	1200 GGCACTGGCCCTCCATCTTCAACAGGCCATGGTCTCTGAGAACAAATGTCATACGGCT 1259
DB	
687 GGCACTGGCCCTCCATCTTCAACAGGCCATGGTCTCTGAGAACAAATGTCATACGGCT 746	
QY	1260 TACCAAATTCAGTGTGAGACACAGTCTGGGCGCATATGAAATACACTGTGGTTTTCT 1319
DB	
747 TACCAAATTCAGTGTGAGACACAGTCTGGGCGCATATGAAATACACTGTGGTTTTCT 806	
QY	1320 GGATACAGAGAGGAATCATCTTGAATCTTTTGGCCGAATTAGAAATACTGGTTTTCT 1379
DB	
807 GGATACAGAGAGGAATCATCTTGAATCTTTTGGCCGAATTAGAAATACTGGTTTTCT 866	
QY	1380 AAATGACAGCCTTTTCTCGAGAGAGATAGTGTTTACAACCTGTAAAAAATGACACTATGA 1439
DB	
867 AAATGACAGCCTTTTCTCGAGAGAGATAGTGTGTTTACAACCTGTAAAAAATGAGACAC 926	
QY	1440 TGGAATCGAAGCAAAAAGATCATGGGCTACAGCTGAGACAGACCAAGCACTCTCTGTA 1499

Db	927	CGCAAAACCTGTAGGGGTTACCATTTATCTTAAACCCCTGGTCAAGCTAGTTTGTGCATCAC	966
QY	1500	TGTTGGCTTCCTACCTGTCGTGATGATTAAGGTTCCCTCGGGCGGGTGAACGACATGGGAA	1559
Db	967	ACTTAGAGAAACAGTGGCTGACGAGAAACATATTTGGTGTCCCGCATATCGTTGCACC	1046
QY	1560	GTTGTAATAAAACCTGTATTGCTCTCCAGAGACCATTATTTGTGATGATTAAGAAAGGTGG	1619
Db	1047	CTTCAATGACACTTTTGTCCATGTCACGTGATCTTTCTGGCAAGAAACCCCTGCCGTGT	1106
QY	1620	TGCGTGCAGCCATTATTCACCCCAACAGCAACACTGACTTTTGACGAGACATATAGCGCTGG	1679
Db	1107	GACTGGTGGATGAAGGTGAAGCGACGACGATGAATCTTTGGCATATGCTGTTATGTT	1166
QY	1680	CAATACAGATGTCCTGGGGGACTGTCTCAATTCCTTTGTGGCACTGATATGGGATTCGAC	1739
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QY	1740	TTCCTCTTGGCCACGACAACACATCAGATTGAGCGCTCAAGAGGGGTATGACTAG	1799
Db	1227	ACACCGGGCCACAGAGAAATAGGACAAGACTCTCGGACCTGGGGCCCAAGTCGGCCCT	1286
QY	1800	GGAGGAAATCTGTGACTGAGAAAGATCTGTTGATCTACCGACAGCAGACA-----	1850
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QY	1851	---CCCTTTGGGGGAGTAGTCTTCCATTAATCACCAAGACAAAGAGGGAGTATTCGGGA	1907
Db	1347	GTCGCCACAAGAGGGGTGTGGGAAATATCCCACTGGAAAGCCAGAGAGTATTCGGGA	1406
QY	1908	AAGTTACTCTAANAAGCCACACCAACGCTGGTTCCCGTACCCCTCTGGSCCAATGACAT	1967
Db	1407	AAGTTACTCTAANAAGCCACGACGACGAGTCCGTCACCTCTGGSCCATGACAT	1466
QY	1968	CCGTGGCTTGGTCATGAGGGGGCCGTCCTCTCGGGGATCAACGCTTACGTGCGTGTGATCA	2027
Db	1467	CTGTGGCTTGGTCATGAGGGGGCCGTCCTCTCGGGGATCAACGCTTACGTGCGTGTGATCA	1526
QY	2028	TGCGCGCAAAAGCTGTGTGTGTGTCAGCGCAGAGAGAGAGCTCACCCACTGTGCGCG	2087
Db	1527	TGCGCGCAAAAGCTGTGTGTGTGTCAGCGCAGAGAGAGAGCTCACCCACTGTGCGCG	1586
QY	2088	GGGCTCATGAGCAGCGCTCACCAAGCTCAGGGGCGCTCTTGGGGGCACTCAATCCAAAGA	2147
Db	1587	GGGCTCATGAGCAGCGCTCACCAAGCTCAGGGGCGCTCTTGGGGGCACTCAATCCAAAGA	1646
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Db	1647	CCCAAAAGCGGAGGCGCATCTCTCACGCGCACTATGCACAAACGCGAAAGCTGCGCACTCCGG	1706
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Db	1707	CAACAAGCGCAAGTGTCTATTAAAGAGACACACACACACCTGTGAGAGGCGCTCCC	1766
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Db	1767	CACCCCAAGTCAACCCCAAGCTGCGAGCAGAACGCGAAGCCCAAGCGCGGAGCGGCA	1826
QY	2328	GTGGGAGAGCAACGAACTCTATCATGCTGCTGCACAAAGACATGCCCCCATGCGCTC	2387
Db	1827	GTGGGAGAGCAACGAACTCTATCATGCTGCTGCACAAAGACATGCCCCCATGCGCTC	1886
QY	2388	CCCTGTGATCCCAAGGACGCTGCCCTGCGGACCTCCCGACGCAATCCCGAGGTGGT	2447
Db	1887	CCCTGTGATCCCAAGGACGCTGCCCTGCGGACCTCCCGACGCAATCCCGAGGTGGT	1948
QY	2448	GGTCTGCGCATCAACGACGAGGGCTACACGATAGTAGTGACCAACCCCAAAATAG	2507
Db	1947	GGTCTGCGCATCAACGACGAGGGCTACACGATAGTAGTGACCAACCCCAAAATAG	2006
QY	2508	CGAGGTGGCCAGATGGCGCTGAGAGACCAAGGCCGCACTGGAGTATTAAGACCATCAA	2567

Db	2007	CGAGGTGGCCCAAGATGGCGCTGGGAGGACAGACGGCCGACACTGGAGATTAAGACCATCA	2086
QY	2568	GGAACATCTCAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAAGCTGGACAG	2627
Db	2067	GGAAACAATCTAGCAGCAAGAGTCCCAACCATGGGGTGAACCTTGTGGAGAAGCTGGACAG	2126
QY	2628	CTTGCCCCCAAGATTCCACAGCGGGAGAGCTCCCTGGGTCCCCGGGAGGCTCCCTGTG	2687
Db	2127	CTTGCCCCCAAGATTCCACAGCGGGAGAGCTCCCTGGGTCCCCGGGAGGCTCCCTGTG	2186
QY	2688	TCAGACCGGTTAAGCAAGGGCTGGAAATCACACACTCCTCTGTCTTACGGGGTTGACTA	2747
Db	2187	TCAGACCGGTTAAGCAAGGGCTGGAAATCACACACTCCTCTGTCTTACGGGGTTGACTA	2246
QY	2748	TAAAGAGAGCTACCCCAAGAACTGCTACAGAAAGCCACCAAGGACCACTCTCAAAAG	2807
Db	2247	TAAAGAGAGCTACCCCAAGAACTGCTACAGAAAGCCACCAAGGACCACTCTCAAAAG	2306
QY	2808	AAACAACTACTACTCTCCAAATTCTCTCACTCTCCAGAAACCAAGAGCTTTGGCAAGGG	2867
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QY	2868	AGACAACCGCGCGCGCGCCGCGCGAGAGGGTGAACCTCATCCAGGCGCAGGTCCACGC	2927
Db	2367	AGACAACCGCGCGCGCGCCGCGCGAGAGGGTGAACCTCATCCAGGCGCAGGTCCACGC	2422
QY	2928	ATCTGGCCAGGCGCGTACTGTCTCGAGGACAGCCAGCCTCAACGCGCTCAACTCACTGAC	2987
Db	2427	ATCTGGCCAGGCGCGTACTGTCTCGAGGACAGCCAGCCTCAACGCGCTCAACTCACTGAC	2486
QY	2988	AAGCTCGGGGCTGAAGCGTACGCCCTGGCTAAAGCGGAGCGTACCCCCCAAAACATCCMT	3047
Db	2487	AAGCTCGGGGCTGAAGCGTACGCCCTGGCTAAAGCGGAGCGTACCCCCCAAAACATCCMT	2546
QY	3048	TGCTGCCCTTTCACATCCATGAAGCCCAATGATCGTGTAATAA 3093	
Db	2547	TGCTGCCCTTTCACATCCATGAAGCCCAATGATCGTGTAATAA 2592	

Search completed: September 30, 2003, 16:58:34
Job time : 808.168 secs

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QY 344 ATGAGTGCACAACTTTATTAAGTCTTCTTAAGAAAAACGATGATGATCTGTCT 403
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QY 464 TGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 523
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Db 476 AGGATGAGAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 535
QY 524 CACTGTTGAGATGAGAAAACTTACTACAGCCAGTGAAGTGAAGTGAAGTGAAG 583
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Db 536 CACTGTTGAGATGAGAAAACTTACTACAGCCAGTGAAGTGAAGTGAAGTGAAG 595
QY 584 CAGTCAATTAACGAGGCTTGGAGAAAGCCCTACCTGGGAGCCGTCAGACGATCA 643
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Db 656 AGTGGCTCGAGAGCCACACTTGTCCAGGCTTGGAGATGAGACATGATGATGAT 715
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Db 1313 TCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1372
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Db 1373 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1429
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Db 1610 GTGAGAGG 1617

RESULT 4
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ. ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ. ID NO 4
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(3432)
; OTHER INFORMATION: Tissue Type: Child Brain
; NAME/KEY: 5'UTR
; LOCATION: (1)-(187)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: misc.feature
; LOCATION: (188)-(2977)
; OTHER INFORMATION: CDS; Identification Method: E
; NAME/KEY: 3'UTR
; LOCATION: (2978)-(3407)
; OTHER INFORMATION: Identification Method: E
; NAME/KEY: polyA.signal
; LOCATION: (3408)-(3432)
; OTHER INFORMATION: Identification Method: E
US-09-254-594-4

Query Match 14.3%; Score 443.6; DB 4; Length 3432;
Best Local Similarity 58.6%; Pred. No. 9.2e-109;
Matches 849; Conservative 0; Mismatches 584; Indels 15; Gaps 4;

QY 164 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 223
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Db 603 GTGAGCAAGCACTATTCAGCCCTGCTGTCGCCAGCACTATGGGATTAATTCCTGCGAGCAGG 662
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QY 1538 GCCGCTGTGAACGATGGAAGTGTAAAAAAAACCTGTATGCTCCAGAGACCCATATT 1587
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 QY 1598 GTGAGATGG 1605
 Db 1797 GTGAGATGG 1804
 RESULT 5
 US-09-254-594-2
 : Sequence 2, Application US/09254594
 : Patent No. 6566094
 : GENERAL INFORMATION:
 : APPLICANT: KIMURA, Toru
 : APPLICANT: KIKUCHI, Kaoru
 : TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
 : FILE REFERENCE: 0020-4527P
 : CURRENT APPLICATION NUMBER: US/09/254,594
 : CURRENT FILING DATE: 1999-05-11
 : NUMBER OF SEQ ID NOS: 13
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 2
 : LENGTH: 2787
 : TYPE: DNA
 : ORGANISM: Rattus norvegicus
 : NAME/KEY: misc.feature
 : LOCATION: (1)..(2787)
 : NAME/KEY: CDS
 : LOCATION: (1)..(2787)
 : OTHER INFORMATION: Tissue Type: Brain
 : OTHER INFORMATION: Identification Method: E
 : NAME/KEY: misc.feature
 : LOCATION: (1)..(1)
 : OTHER INFORMATION: Identification Method: P for resulting peptide
 : US-09-254-594-2
 Query Match 12.0%; Score 369.8; DB 4; Length 2787;
 Best Local Similarity 55.9%; Pred. No. 5e-89;
 Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;
 QY 164 GCGTGACATCCAGATGATTTATGATCATGAGACGGAACCTCTACTGTTGCTGAGGAGC 223
 Db 176 GCGTGACATCCAGATGATTTATGATCATGAGACGGAACCTCTACTGTTGCTGAGGAGC 235
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 Db 473 AGGGAGAGAGGCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 532
 QY 524 CACTGTTTCAATGAGAAACATATACCTGAGGAGAGTACTGATGATGATGATGATGAT 583
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 QY 584 CAGTATTTACGAGAGTGTGAGAAAGCCCTACCTGCGGAGCCGTCAAGACAGATTCAA 643

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DB 653 AGTGGCTCGAGACCACTTGTCTATGCTTGGAGCATGAGACCATCTACTTCT 712
QY 704 TCTTCAGGAAATAGCAGTGAATAT--ACACCATGGGAAAGTATTTCCCAAG 760
DB 713 TTTCTCCGAGAAATCTCTGTGGAGGAGCCCGGCTGGGGAGGATTCAGTTTCCGG 772
QY 761 TGGCTCAGTTTGTAAAGATATATGGAGAGATCTCAAGAGCTCTGAGAAACATGGA 820
DB 773 TGGCCCGGAGTGTAAAGCTACATGGGTGCTCACCAGGCGCTTGATGCCACATGA 832
QY 821 CGTGTCTTCAAGAGCGGCTTGAAGCTGCTCAGTTCTGAGACTCTCATTTTATTTCA 880
DB 833 CATCTTCTTAACTGAGCTCAAGTCTCCGTCCTGGGAGCATCTTACCTTACCTTTG 892
QY 881 ACATTTCCAGGAGCTTACAGATGATGCTGATCAACAGGCGCTGATGTTTCCCGCA 940
DB 893 ATGCTTACAGTCTTAACTGGGCTGTAAGCTGACATGGGCTGCTCCCTTTGGGG 952
QY 941 CGTTTCTACACTTAAACAGCATCCCTGGGCTGAGCTGTGCTATGACATGCTTG 1000
DB 953 TCTTACTACTCAGACCATAGCATCTCTGGGCTGCGAGCTGCGGCTTACCTAGATG 1012
QY 1001 ACATTTCCAGTGTTTTACTGAGGAGTTCAGAGAAAGAGTCTCTGATTTCCACCTGA 1060
DB 1013 ACATTTGAAGCTGTGTGAGGAGCAAGTTCAGAGAGAGAGTCTGATGGGCTGGA 1072
QY 1061 CACCACTTCTGATGAGAGATCTCTAGCCAGGCGGAGTGGCTGCTGGCTCATCT 1120
DB 1073 CTCTGTCTGAGAGCAAAATCTCCCTCACCAGGCGGAGTCTGCTGAGGCTG 1132
QY 1121 CCTTGAAGATATGCACTTCAATGAGTCCCTGATGATACCTGTAATCATCAAGA 1180
DB 1133 CAGCTGCTTATCTCTCTCTCTCTCAAGACCTGCTGAGAGTGTCTGCTTCAATCAAG 1192
QY 1181 GCGACCGGCTCATGATGAGGAGTGGCTCCATCTTCAAGAGGCGATGCTCTGAGGA 1240
DB 1193 CACACCGACCTGTGATCCCGCTGTGCCACC--TGCCACCCATCAACCTCTCCCTCATCT 1249
QY 1241 CAATGCTGAGATACCGCTTACCAAAATTTGACATGAGGAGACAGCTCTGGGCGATTCAGA 1300
DB 1250 TGACTAGAGGAGCTTACTGACCCAGTACTGTGATGATGCTGAGGCTGAGGCTGAG 1309
QY 1301 ATCACACTGTGTTTCTTGGGATCAGAGAAAGGAGATCATCTTGAATTTTGGCCAGAA 1360
DB 1310 ATACTACAGTCTCTGTTCTGTGCTCCATGATGAGGAGAGTGTGAGGCTGAGCTGAG 1369
QY 1361 TAGGAATATGAGTGTCTTAAATGACAGGCTTTCTCTGAGAGAGATGATGTTTACACT 1420
DB 1370 GGGGACA--GTCTGTGGAGACCCGAGCCATATCATTTGGAAGATGATGATGCTTCAAG 1426
QY 1421 CTTGAAAAATGACAGTATGATG--AGTGAAGACAAAAGGATCATGGGCTGACAGC 1474
DB 1427 ATGCCCCGTGAGTGGAGAGCGGTACCCCGAGCTGCTGACGAGATCATAGGCGTGGAGC 1486
QY 1475 TGGAGAGAGCAAGCACTCTGTATGTTGCGTTCTTCACTGTGTATAAAGTGTCC 1534
DB 1487 TGGACACATGAGGCTTACAGGCTTTTGTGGCTTCTGATGATGATGCTGCTGCTG 1546
QY 1535 TTGGCCGCTGTAGAGAGATGAGGAGTGTAAAAAAGCTGTATGCTTCCAGAGAGCCAT 1594
DB 1547 TTAGCGGCTGTGCTCCGCGATGAGGAGATGAGGAGGCTGCTGCTTCTGAGCCCAT 1606
QY 1595 ATGTTGATGG 1605
DB 1607 ACTGTGATGG 1617

RESULT 6
US-09-254-594-1

Sequence 1, Application US/09254594
Patent No. 6566094
GENERAL INFORMATION:
APPLICANT: KIMCHI, Toru
APPLICANT: KIMCHI, Kaoru
TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
FILE REFERENCE: 0020-4527P
CURRENT FILING DATE: 1999-05-11
CURRENT FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 3195
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(3195)
OTHER INFORMATION: Tissue Type: Brain
NAME/KEY: 5'UTR
LOCATION: (1)..(50)
OTHER INFORMATION: Identification Method: E
NAME/KEY: misc_feature
LOCATION: (51)..(2837)
OTHER INFORMATION: CDS; Identification Method: E
NAME/KEY: 3'UTR
LOCATION: (2838)..(3195)
OTHER INFORMATION: Identification Method: E
US-09-254-594-1

Query Match 12.0%; Score 369.8; DB 4; Length 3195;
Best Local Similarity 55.9%; Pred. No. 5.4e-89;
Matches 811; Conservative 0; Mismatches 622; Indels 18; Gaps 5;

164 GCGTGGACATCCAGATGATATGATCATGAAACGAGACCTTACTATGCTGAGGAGC 223
DB 226 GAGCTGACTTTCAGAGATTCCTGAGCTTGAACCGGAGCCTTGTGTGCTGCGGAGTC 285
QY 224 ATATTATATCTGTATATATGACATGACATGACACGAGAAATTTATGTAGCAAAAAC 283
DB 286 AGCTTTCTCTGATCTTCAAGCCCAAGAGAGAGAGGAGGCTGCTGCTTCAAGT 345
DB 284 TGACATGGAATCTAGAGAGGCGGATGAGACATGACATGAGAGGAGAAACATTAAG 343
DB 346 T---TCTGACATGGGAGGAGCCAGACATGAGATATGCTGCTGCGGAGAGCTGAGCG 402
QY 344 ATGATGCCACACTTTATTAAGTTCTTCTTAAAGAAAACCATGATGATGTTGTCT 403
DB 403 ACGAATGCTACAACTACATCCGCTGTCTTCTTCCCTGAGCTGCGAGATCTGCTGCT 462
QY 404 GTGGAACATATGCTTCAACCTTCTCTGAGAACTATTAAGATGATATGATGAGACAT 463
DB 463 GTGGAACATATCTTACAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTGAGCTTCTG 522
QY 464 TCGGGAGTAAATTCAGCGGAGATGCGGAGATGCCATGATGATGCCAATATGCCAGCTG 523
DB 522 AGGGTGAAGAGCTGATGAGGAGCTGAGCTGAGCTTCTGATGATGATGATGATG 582
QY 524 CACTGTTTGAATGGAATATGATGATGATGATGATGATGATGATGATGATGATGATG 583
DB 583 CCATCTCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 642
QY 584 CAGTCAATTAACCGAGTCTTGGAGAAAGCCCTACCTTGGGAGCCGTCAGACAGATTCAA 643
DB 643 CTGTGTTTACAGAAAGCCCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTTGGAGCTT 702
QY 644 AATGTTGAAGAACATCTTGTTCAGAGCCGCTGATATGAGAGATATATCTACTCT 703
DB 703 AGTGGCTTGAAGAGCCACATCTTGTATGCTTGTGAGATGAGAGCCATGCTACTTCT 762
QY 704 TCTTCAGGAAATGAGAGTGAATAT--ACACCATGGGAAAGTATTTCCCAAGAG 760
DB 763 TTTCTCCGAGAAATCTCTGTGGAGGAGCCCGGCTGGGGAGGATTCAGTTTCCGG 822

761 TGGCTCAGGTTTGGTAAGATATATGAGGAGATCTCAAGAGNCTGGAGAACAGTGA 820
823 TGGCCCGGGGTGTAAACGTAGATGAGGATGGCTACACGCGGCTTGAGATCGCACATGA 882
821 CGTGTCTCCGAAGAGGCGCTGTAAGCTGCTCACTTCTGAGAGCTGCTATTATTTCA 880
883 CATCTCTCTTAAGAGGAGCTCAACGCTCCGTCCTGGGAGCTGCTACTTCTACTTTG 942
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943 ATGTCTTACAGTCTTAACTAGGCGCTGTGAACCTGTGATGGCGCTGCGCTTTGGGG 1002
941 CGTTTCTACACCTTAAACGATCCCTGGTCTGCTGAGCTGCTGCTATGATGATGCT 1000
1003 TCTTCACTACTCAACCAATGACATGCTGCTGGGTGTGAGTCTGCGCTTCTACTGATG 1062
1001 ACATTGCAAGTCTTTTACTGAGAGATTCAGAGAGAGAGATGCTGATTCACCTGGA 1060
1063 ACATTGAGAGTGGCTTTGAGGAGAGATTCAGAGAGAGAGATGATGGAGGCGCTGGA 1122
1061 CACCACTTCTGTATGAACAGTTCCTAAGCCGAGGCTGCTGCTGCTGCTCATCT 1120
1123 CTCTGTGTCTGAGGACAAAGTCCCTCAACCCAGGCGGCTGCTGTGAGGTGAGGTG 1182
1121 CCTTGAAGATATGACACCTCAAGAGTTCCTGATGATGATGATGATGATGATGATG 1180
1183 CAGCTGCTTATCTCTCTCTCTCAACAGCTGCTGAGAGATGCTGCTGCTGCTGATCAG 1242
1181 CGCAGCCGCTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1240
1243 CACACCCAGTGTGATCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
1241 CATTGCTCAATACCGCTTACCAAAATTCAGATGAGAGAGAGAGAGAGAGAGAGAG 1300
1300 TGACTGACAGGCTCTACTGATGACCCAGTACTGCTGATGCTGCTGCTGCTGCTGCT 1359
1301 ATACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1360
1360 ATACTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1419
1361 TAGGAATAGTGTGTTCTTAATGACAGCTTTTCTGAGAGAGATGATGTTTACACT 1420
1420 GGGGACA--GTCCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1476
1421 CTGAAAATGACAGTATGATGAGG-----AGTGAAGAGAGAGAGAGAGAGAGAGAG 1474
1477 ATGCGCGGTGAGTGGAG 1536
1475 TGGACAG 1534
1537 TGGACACTGAG 1596
1535 TTGGCGCGGTGAG 1594
1597 TCACCCGCTGTGCGCGGAGATGAGAGATGACAGAGAGAGAGAGAGAGAGAGAGAG 1656
1595 ATTGTGATGAG 1605
1657 ACTGTGATGAG 1657

RESULT 7
US-08-121-713D-57
Sequence 517, Application US/08121713D
Patent No. 5639856
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Mathes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY IAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121/713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 2854 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 451..2640
US-08-121-713D-57
Query Match 5.4%; Score 166; DB 1; Length 2854;
Best Local Similarity 53.0%; Pred. No. 2.2e-34;
Matches 532; Conservative 0; Mismatches 415; Indels 57; Gaps 6;
289 TGGAAATCTAGACAGGCGCGATGTGACACATGACAGATGAGAGAGAGAGAGAGAG 348
709 TGGCAGCTGTCAGAGTGGCCATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
349 TGGCAGCACTTATTAAAGTCTCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 408
769 TGGCAGAGATCATCATCCGAGTCTGCGCAAAATGACATGACCGCGATCTGCGGT 828
409 ACTAATGCTTCAACCTTCTGCAAGAACTATAGAT--GATATATTGGAACATTC 465
829 ACGAAGCCCTATAG 888
466 GGGGATGATTCACCGAG 525
889 GAGAAAGATATGAG 948
526 CTGTTGAGATGAG 585
949 ATATACAGTGGAG 1008
586 GTCAATTACCGGAGTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 645
1009 CTCAATACCGCGGCC-----CTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1053
646 TGGTTGAAG 705
1054 CAATTAAATGCTCTTAATCTTGTCAACAGATGAGATGATTAATTAATTTCTTCTC 1113
706 TTCAAGGAG 765
1114 TTCGAG 1173


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QY 766 CAGTTGTAGATGATGAGATGATCTCAAGAGTCTCGAGAGAAACAGTGCAGTCG 825
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1174 AGAGTCTGTAAACATGACAGAGGCGCCCTCATCAGGCTGTGACAGA---TGGACTTCT 1230
QY 826 TTCCTGAAGCGCGCTTGAACCTGCTGATGCTCGAGACATCTCATTTTATTTCAACATT 885
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1231 TTTTGAATACAGCTGTGAAGTGTTCGCTCCCTGGAGATTTATCATTTTACTTCAATGAA 1290
QY 886 CTCAGGACATTTACAGATGTGATTCGTATACAGGCGCGTATGTTCTCTGCGAAC--- 941
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1291 ATTGAGTCAACAGTACATCATTTGAAGAAATTTATGTTGCTCAAGGAGAAATCATC 1350
QY 942 -----GTTTCTACACCTTAAACAGATCCCTGGGCTGTGAGCTGTGCTATGAC 993
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1351 TACGGTCTTTCAGACACCAAGTACATCTTATGTTGCTGTCTGTGTTTGTGCTTCACT 1410
QY 994 ATGCTTGACATTTGCCATGTTTATCTGAGAGATTCAGAGACAGAAATCTGATTC 1053
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1411 ATGAGTCAATCTGATGATGATTTGATGTCATTTTAAAGAGAGAAACGATGAACTCA 1470
QY 1054 ACCTGACACGAGTCTGATGAAACGAGTTCCTAAGCCAGCCAGCTGCTGTCTGCGC 1113
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1471 AACTGTTGGCAGAGCCAGACCTTAAAGTCCAGAACCAAGGCTGAGCAATGTGT--- 1526
QY 1114 TCATCCCTCTTGAAGATATGCAACCTCCATGATGCTGCTGATGATACCTGAACTTC 1173
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1527 -----GATACAGCTGTACAC-----TTCCTGATGTTGCTGTCAATTTT 1566
QY 1174 ATCAAGACGACCGCTCATGATGATGAGCAGATGCGCTCATCTTCAACAGGCCATGCTC 1233
  || || || || || || || || || || || || || || || || || || || || || ||
Db 1567 GTAAAGTCAATACACTGATGATGATGAGGCGCGCTGACCATTTTACTCGGCCAATCTC 1626
QY 1234 CTGGAACATGTGACATACCGCTTACCAAAATTCAGATGGA 1277
Db 1627 ATTGAGTACGCTTACAGTACAGATTTCAAAATATGCTGTGA 1670

```

RESULT 8

US-08-835-268-57

Sequence 57, Application US/08835268

Patent No. 5807826

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/835,268

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Osmen, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

```

: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
:
: INFORMATION FOR SEQ ID NO: 57:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2854 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 451..2640
: US-08-835-268-57

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Query Match

Best Local Similarity 53.0%; Pred.No. 2.2e-34;

Matches 532; Conservative 0; Mismatches 415; Indels 57; Gaps 6;

5.48; Score 166; DB 1; Length 2854;

289 TGGAAATCTAGACAGCGCGATGTAGACACATGCAATGGAAGGAAACATTAAGATGAG 348

709 TGGACTGCTGACAGTGGCCATCGGAGCTCTGCTACTCAAGGGAAGTCAAGAGAGAC 768

349 TGGCACAATTTTATTAAGTCTCTTAAAGAAAACGATGATGATTTGTTGTGGA 408

769 TGGCAGAACATACATCCAGTCTGCGAATTAAGCATGACCGGATGATGATGATGATG 828

409 ACTATACCTTCAACCTCTCTCTGAGAACTATTAAGT---GATATATTGAAACATTC 465

829 ACGAAGCTATTAAGCCATGATGAGGACCTGACCTCAAGATGAGATTAATTTGTA 888

466 GGGATGATTAAGCGGAAATGAGGAGATGCGCATATGATGCAACATGCAACAGTTGCA 525

889 GAGAAAGATATGAGGAAAGATTTGGCCATTTAGCCTTACACCAACAGACATGCA 948

526 CTGTTTGCAGATGAGAAATCTATCTACGCCAGTACTGCTCTTCCATTTGACGCA 585

949 ATATACAGTAGAGGACATTTGATCTACGAAAGTGGACAGACTCTCTGGAACAGACCT 1008

586 GTCAATTACCGGATCTTGGAGAAAGCCCTAACCTGGGAGCCGTCAGACAGATTCAAA 645

1009 CTCATATACCGGCGC-----CTTAAAGAACAGAGATCTGACCTCAAA 1053

646 TGGTTGAAGAACCATATTGTTCAAGCGGTGATTACGAGATTAATATCTACTCTTC 705

1054 CAATTAATGCTCTTACTTGTCAACACATGAGATGATTTATTTATTTCTCTTC 1113

706 TTCAGGAAATAGCAGTGAATATACATGAGGAAAGTATGTTTCCAAAGTGGCT 765

1114 TTCGAGAGACTGCTGTGATGATCATCAACGCGGAAAGGCTATCTATCAAGGTTGCC 1173

766 CAGTTGTAGATGATGAGATGAGGAGATCTCAAGAGATCTGAGAAACAGTGCAGTCG 825

1174 AGAGTCTGTAAACATGACAGAGGCGCCCTCATCAGGCTGTGACAGA---TGGACTTCT 1230

826 TTCCTGAAGCGCGCTTGAACCTGCTGATGCTCGAGACATCTCATTTTATTTCAACTT 885

1231 TTTTGAATACAGCTGTGAAGTGTTCGCTCCCTGGAGATTTATCATTTTACTTCAATGAA 1290

886 CTCAGGACATTTACAGATGTGATTCGTATACAGGCGGCTGATGTTCTCTGCGAAC--- 941

1291 ATTGAGTCAACAGTACATCATTTGAAGAAATTTATGTTGCTCAAGTGAAGAACTATC 1350

942 -----GTTTCTACACCTTAAACAGATCCCTGGGCTGTGAGCTGTGCTATGAC 993

1351 TACGGTCTTTCAGACACCAAGTACATCTTATGTTGCTGTGCTGTGTTGCTTCACT 1410

994 ATGCTTGACATTTGCCATGTTTATCTGAGAGATTCAGAGACAGAAATCTCTGATTC 1053

1411 ATGAGTCAATCTGAGTCAATTTGATGTTGCTCAATTTTAAAGGAGGAAACGATGAACTCA 1470

1054 ACCTGACACAGTTCCTGATGAGAGATTCCTAAGCCAGGAGGTTGCTGTGCTGCGC 1113

Db 407 GCGTGGCCGCGCTGCAATGAGGACAAAGTGCGCCGATCATTC---GCAACGCT 463
 QY 818 GAGAGTGTCTCGAAGGCGCGCTTGAAGCTGCTGCTGAGACTCATTTTATT 877
 Db 464 GGAATCTCTCCCAATCCCGCTCAACGCTCAATCCCGGATTAATCTTTACT 523
 QY 878 TCAACATCTCCAGGAGTATGATGTAT-----TCGATCAACGGGCGTG 925
 Db 524 TTAATGAATCCAAATCTGCCAGCAATCTGTTGAGAGGAGACGTATGCTCATGACGCGA 583
 QY 926 ATGTGCTGCGGACAGCTTTTCTACACCTTATACAGCAATCCCTGGCTGACGTCTG 985
 Db 584 AACTGATCTAGGAGTCTTCAACACGCGAGCAACTCAATCCCGGCTGACGCTTG 643
 QY 986 CCTATGACATGCTTGAATGCTGCTGCTTTTACTGAGAAATTCAGAGACAGACTCTC 1045
 Db 644 CCTTGGCCCTCCAGGACATTTGCGATACGTTGAGGCTCAGTCCAAAGACAGACTGGA 703
 QY 1046 CTGATTCACCTGAGACACGCTTCTGATGAGAGCTTCTAAGCCCGACAGCTTGTCT 1105
 Db 704 TCAACTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
 QY 1106 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
 Db 764 GTCAACAGATTCG-----AGAGCGCTTCCGGATCCGACAC 799
 QY 1166 TGAATCTGATCAGACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1225
 Db 800 TGAATCTGATCAGACAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 859
 QY 1226 CAGTCTCTGAGACAAATGCTGATGAGAGCTTCTAAGAAATTCAGAGTGA 1277
 Db 860 CGATTCTGCTGAGACAAATGCTGATGAGAGCTTCTAAGAAATTCAGAGTGA 911

RESULT 14

US-08-835-268-59
 : Sequence 59, Application US/08835268
 : Patent No. 5807826

GENERAL INFORMATION:

: APPLICANT: Goodman, Corey S.
 : APPLICANT: Kolodkin, Alex L.
 : APPLICANT: Mathes, David
 : APPLICANT: Bentley, David R.
 : APPLICANT: O'Connor, Timothy
 : TITLE OF INVENTION: The Semaphorin Gene Family
 : NUMBER OF SEQUENCES: 100
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 : STREET: 268 Bush Street, Suite 3200
 : CITY: San Francisco
 : STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/835, 268

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/121, 713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

: TELEFAX: (415) 343-4342
 : TELETYPE:
 : INFORMATION FOR SEQ ID NO: 59:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 3560 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 1..1953
 : US-08-835-268-59
 Query Match 4.7%; Score 146.4; DB 1; Length 3560;
 Best Local Similarity 51.9%; Pred. No. 4.4e-29;
 Matches 494; Conservative 0; Mismatches 401; Indels 57; Gaps 5;
 Db 401 TCTGTGGAATGATGCTTCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 457
 QY 401 TCTGTGGAATGATGCTTCAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 457
 Db 62 TTTGTGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 QY 62 TTTGTGCAACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
 Db 458 AACCATTCGGGATGAAATTCAGCGAATGCGAGATGCGCATATGATGCGCAACATGCCA 517
 QY 458 AACCATTCGGGATGAAATTCAGCGAATGCGAGATGCGCATATGATGCGCAACATGCCA 517
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 QY 122 ACAGCTGAGAGGCCACGAAAGAGACAGAGCGGATGTCGCTTACGATCCAGTCACT 181
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 QY 182 CCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241
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 QY 578 TTGACGAGCTATTCAGGAGCTTGGAGAAAGCCCTACCTGCGGAGCGTCAAGCAG 637
 Db 242 GCGATCCGATTAATCTACCGGAGC-----CCCTGAGACCGAGCAGTAC 286
 QY 242 GCGATCCGATTAATCTACCGGAGC-----CCCTGAGACCGAGCAGTAC 286
 Db 638 ATTCAAAATGCTTGAAGAACCACTTTGCTTCAAGCCGCTGATTAAGAGATTAATCT 697
 QY 638 ATTCAAAATGCTTGAAGAACCACTTTGCTTCAAGCCGCTGATTAAGAGATTAATCT 697
 Db 287 ATAGCTTAAGCTCAACGACCGAATCTTGGAGCTCAATTAACGAGGCGCATTTGCT 346
 QY 287 ATAGCTTAAGCTCAACGACCGAATCTTGGAGCTCAATTAACGAGGCGCATTTGCT 346
 Db 698 ACTTCTTCTTGAAGAAATACAGTGGAGTATTAACAGATGGAAGGAGTATTCCTCCAA 757
 QY 698 ACTTCTTCTTGAAGAAATACAGTGGAGTATTAACAGATGGAAGGAGTATTCCTCCAA 757
 Db 347 ATTCTCTTTCGGGAAACCGCGTGGATTAATCACTGAGGACGAGATTTTTC 406
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 Db 758 GAGTGGCTCAGCTTGTGAAGATGATGAGAGATTCCTCAAGAGTCTGAGAGAAACAGT 817
 QY 758 GAGTGGCTCAGCTTGTGAAGATGATGAGAGATTCCTCAAGAGTCTGAGAGAAACAGT 817
 Db 407 GCGTGGCCGCGCTGCAATGAGGACAAAGTGGCGCCGATCATGCTC---GCAACGCT 463
 QY 407 GCGTGGCCGCGCTGCAATGAGGACAAAGTGGCGCCGATCATGCTC---GCAACGCT 463
 Db 818 GAGAGCTGCTTCTGAAGGCGGCTTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
 QY 818 GAGAGCTGCTTCTGAAGGCGGCTTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 877
 Db 464 GGAATCTCTCTCAAGTCCCGCTCAACCTGCTCATTCGCGGATTAATCTTTTACT 523
 QY 464 GGAATCTCTCTCAAGTCCCGCTCAACCTGCTCATTCGCGGATTAATCTTTTACT 523
 Db 878 TCAACATCTCCAGGAGTATGATGTAT-----TCGATCAACGGGCGTG 925
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 Db 524 TTAATGAATCCAAATCTGCCAGCAATCTGTTGAGAGGAGACGTATGCTCATGACGCGA 583
 QY 524 TTAATGAATCCAAATCTGCCAGCAATCTGTTGAGAGGAGACGTATGCTCATGACGCGA 583
 Db 926 ATGTGCTGCGGACAGCTTTTCTACACCTTATACAGCAATCCCTGGCTGACGTCTG 985
 QY 926 ATGTGCTGCGGACAGCTTTTCTACACCTTATACAGCAATCCCTGGCTGACGTCTG 985
 Db 584 AACTGATCTAGGAGTCTTCAACACGCGAGCAACTCAATCCCGGCTGACGCTTG 643
 QY 584 AACTGATCTAGGAGTCTTCAACACGCGAGCAACTCAATCCCGGCTGACGCTTG 643
 Db 986 CCTATGACATGCTTGAATGCTGCTGCTTTTACTGAGAAATTCAGAGACAGACTCTC 1045
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Db 2074 GCACTGCTTTCCTCATATACCAAGACAGCAAGAGGAGTATTCGGAAAGTTACTCTCAA 2133
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Db 1630 AATGACAGCCTTTTCCTGGAGGAGATGAGTGTTCACAACTCTGAAAATGCGAGCTATGAT 16

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3
4
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RESULT 4			
US-09-991-053-5			
: Sequence 5, Application US/09991053			
: Publication No. US20030003532A1			
: GENERAL INFORMATION:			
: APPLICANT: Shinketsu, Richard A.			
: TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-1,			
: TITLE OF INVENTION: MEGF-1 AND ROUNDABOUT-LIKE POLYPEPTIDES			
: FILE REFERENCE: 15966-540 CON S-10			
: CURRENT APPLICATION NUMBER: US/09/991-053			
: PRIOR FILING DATE: 2002-05-23			
: PRIOR APPLICATION NUMBER: USSN 60/123,667			
: PRIOR FILING DATE: 1999-03-09			
: PRIOR APPLICATION NUMBER: 09/520,781			
: PRIOR FILING DATE: 2000-03-08			
: NUMBER OF SEQ ID NOS: 81			
: SOFTWARE: PatentIn Ver. 2.1			
: SEQ ID NO 5			
: LENGTH: 3333			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: CDS			
: LOCATION: (214)..(2865)			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (2882)			
: OTHER INFORMATION: an n may be any one of a or t or g or c			
: US-09-991-053-5			

Query Match 87.2%; Score 2698; DB 11; Length 3333;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;

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 1834 GCGTGCAGCCATTTTCAACCCACAGCAGACTGACTTTTGGACAGACATAGAGGTGC 1893
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 1894 AATACAGATGCTGGGGAGCTGTCAATTCCTTTTGGGCACTGAAT 1941
 1741 TCCCTCTTCCAGCACAACCAATCAGATTGACGGGCTCAAGAGGGATAGTCTAG 1800
 1942 TCCCTCTTCCAGCACAACCAATCAGATTGACGGGCTCAAGAGGGATAGTCTAG 1941
 1801 GGAGAGATGCTGGACTGGAAGCATCTGTTGACTCACTGACAGCAGACAGCCCTTGGGG 1860
 1942 GGAGAGATGCTGGACTGGAAGCATCTGTTGACTCACTGACAGCAGACAGCCCTTGGGG 1941
 1861 GCAAGTCTCTCCATTAATTCACAAGACAAGAGAGATTCGGGAAGTAACTCAAA 1920
 1942 GCAAGTCTCTCCATTAATTCACAAGACAAGAGAGATTCGGGAAGTAACTCAAA 1968
 1921 GGCACAGACCACTGGTTCGCCGCAACCCCTTGGCCATGACATCTGCTGCTTCGTC 1980
 1969 GGCACAGACCACTGGTTCGCCGCAACCCCTTGGCCATGACATCTGCTGCTTCGTC 2028
 2029 ATGGGGGCGCTCTTCCGSGGCAACACCGTCTACTGCTGTGATCATGGGGCAAGAC 2088
 1981 ATGGGGGCGCTCTTCCGSGGCAACACCGTCTACTGCTGTGATCATGGGGCAAGAC 2040
 2041 GTGGCTGTGGTCAAGCGCAAGAGAGAGTCAACCACTCGCGCGGGGCTCCATAGAGC 2100
 2089 GTGGCTGTGGTCAAGCGCAAGAGAGAGTCAACCACTCGCGCGGGGCTCCATAGAGC 2148
 2101 AGCGTCACCAAGCTGACGGGCTCTTGTGGGACACTCAATCCAAAGACCCAAAGCCGGAG 2160

Db 2149 AGGTCACCAAGTCTAGCGGCTCTTTGGGAGACACTAATCCAAAGCCAAAGCCGGAG 2208
 QY 2161 GCCATCTCAGCGCACTCATGACAAAGGCAAGCTCGCCACTCCCGCAACAGGCGCAAG 2220
 Db 2209 GCCATCTCAGCGCACTCATGACAAAGGCAAGCTCGCCACTCCCGCAACAGGCGCAAG 2268
 QY 2221 ATGCTATTAAAGCAACCAAGCAACCACTGAGCTTACAGGCGCTCCCGCAACAGGCTA 2280
 Db 2269 ATGCTATTAAAGCAACCAAGCAACCACTGAGCTTACAGGCGCTCCCGCAACAGGCTA 2328
 QY 2281 ACCCAAGCGTGCAGAGAGAGAGGCGGAGCCAGCGCGGAGCGGAGGAGGAGAGAGAG 2340
 Db 2329 ACCCAAGCGTGCAGAGAGAGAGGCGGAGCCAGCGCGGAGCGGAGGAGGAGAGAGAG 2388
 QY 2341 CAGAACCTCATCAATGCTGCTGACCAAGAGACATGCCCCCAGATGGGCTCCCTGTATGCC 2400
 Db 2389 CAGAACCTCATCAATGCTGCTGACCAAGAGACATGCCCCCAGATGGGCTCCCTGTATGCC 2448
 QY 2401 AGGAGACTGCGCTCTGGGGGCTCTCCCGCAAGCAATCCCGAGGCTGGTGGTCCCGCATC 2460
 Db 2449 AGGAGACTGCGCTCTGGGGGCTCTCCCGCAAGCAATCCCGAGGCTGGTGGTCCCGCATC 2508
 QY 2461 AGCAGACAGGCTACACAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
 Db 2509 AGCAGACAGGCTACACAGCATGATGATGATGATGATGATGATGATGATGATGATGATG 2568
 QY 2521 ATGGCGCTGAGAGACCAAGGCGCGCCACACTGAGTATAGACCATCAAGACATCTGACG 2580
 Db 2569 ATGGCGCTGAGAGACCAAGGCGCGCCACACTGAGTATAGACCATCAAGACATCTGACG 2628
 QY 2581 AGCAAGATGCCCAACCATGGGGGAGAACCTTGTGAGAGAACCTGGAGACGCTGGCGCCAAA 2640
 Db 2629 AGCAAGATGCCCAACCATGGGGGAGAACCTTGTGAGAGAACCTGGAGACGCTGGCGCCAAA 2688
 QY 2641 GTTCCACAGGCGGAGGCGCTCCCTGGGCTCCCGGAGACCTCCCTGCTCAGACGCGCTA 2700
 Db 2689 GTTCCACAGGCGGAGGCGCTCCCTGGGCTCCCGGAGACCTCCCTGCTCAGACGCGCTA 2748
 QY 2701 AGCAAGGCGCTGGAATGACACCACTCTTCTTCTAGCGGCTTGAATTAAGAGAGCTAC 2760
 Db 2749 AGCAAGGCGCTGGAATGACACCACTCTTCTTCTAGCGGCTTGAATTAAGAGAGCTAC 2808
 QY 2761 CCCAGCAAGTCCGACAG 2819
 Db 2809 CCCAGCAAGTCCGACAG 2868
 QY 2820 CTCTCCCAATTCCTCTC-ACCTCTCCAGAAACAGAGCTTTGGCAGGAGAGAGAGAGAG 2878
 Db 2869 CTCTCCCAATTCCTCTC-ACCTCTCCAGAAACAGAGCTTTGGCAGGAGAGAGAGAGAG 2928
 QY 2879 CGCGCGCGCGGAG 2938
 Db 2929 CGCGCGCGCGGAG 2988
 QY 2939 CGGAGCTGCTCAG 2998
 Db 2989 CGGAGCTGCTCAG 3048
 QY 2999 TGAAGCGTACGCGCTCGCTAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3058
 Db 3049 TGAAGCGTACGCGCTCGCTAAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3108
 QY 3059 CCACATCCATGAAGCGCCATGATGCGGTACATAA 3093
 Db 3109 CCACATCCATGAAGCGCCATGATGCGGTACATAA 3143

RESULT 5
 US-09-957-187-5
 ; Sequence 5, Application US/09957187
 ; Publication No. US20030054514A1
 ; GENERAL INFORMATION:

; APPLICANT: Shimkets, Richard A
 ; APPLICANT: Laroche, William
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
 ; FILE REFERENCE: 15966-540 CIP
 ; CURRENT APPLICATION NUMBER: US/09/957,187
 ; CURRENT FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/123,667
 ; PRIOR FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: 09/520,781
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/234,082
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 60/233,798
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 60/174,485
 ; PRIOR FILING DATE: 2000-01-04
 ; NUMBER OF SEQ ID NOS: 85
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 3333
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (214)..(2865)
 ; NAME/KEY: misc feature
 ; LOCATION: (2882)
 ; OTHER INFORMATION: an n may be any one of a or t or g or c
 US-09-957-187-5
 Query Match 87.2%; Score 2698; DB 11; Length 3333;
 Best Local Similarity 93.9%; Pred. No. 0;
 Matches 2907; Conservative 0; Mismatches 21; Indels 167; Gaps 3;
 QY 1 ATGAGTCAAGAGCTTGTCTGCTATATTTACACTGTAACCTTGTGGGCTGGCTTC 60
 Db 214 ATGAGTCAAGAGCTTGTCTGCTATATTTACACTGTAACCTTGTGGGCTGGCTTC 273
 QY 61 CCAGAAATTCCTGAGCCATACATGATTTGCGATGCGCACTATACAAACAGATCCGATG 120
 Db 274 CCAGAAATTCCTGAGCCATACATGATTTGCGATGCGCACTATACAAACAGATCCGATG 333
 QY 121 TTTGTGGGCAAGAGCCAGGAGGAGACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
 Db 334 TTTGTGGGCAAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393
 QY 181 ATTATGATCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
 Db 394 ATTATGATCATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 453
 QY 241 ATAGACATCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
 Db 454 ATAGACATCATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 513
 QY 301 CAGGCGGATGAGACATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
 Db 514 CAGGCGGATGAGACATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 573
 QY 361 ATTAAGTCTTCTTAAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
 Db 574 ATTAAGTCTTCTTAAGAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 633
 QY 421 AACCTTCTCTCAGAAATATATAGATGATGATGATGATGATGATGATGATGATGATGAT 480
 Db 634 AACCTTCTCTCAGAAATATATAGATGATGATGATGATGATGATGATGATGATGATGAT 693
 QY 481 GGAATGCGCAGATGCCATATATAGATGATGATGATGATGATGATGATGATGATGATGAT 540
 Db 694 GGAATGCGCAGATGCCATATATAGATGATGATGATGATGATGATGATGATGATGATGAT 753
 QY 541 AAATATATCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 Db 754 AAATATATCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 813


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|||||
Db 1081 AGATATGCAACCTCCATGAGTCCCGATGATACCTGAACTCAATCAAGACGACCG 1140
QY 1189 CTCATGATGAGGAGTGGCTCCATCTTCAACGAGGCGATGTTCTCGAAGACATGTC 1248
Db 1141 CTCATGATGAGGAGTGGCTCCATCTTCAACGAGGCGATGTTCTCGAAGACATGTC 1200
QY 1249 AGATACCGGCTTACCAAAATTCAGTGGACACAGCTGCTGGCCCATATCAGATCAGACT 1308
Db 1201 AGATACCGGCTTACCAAAATTCAGTGGACACAGCTGCTGGCCCATATCAGATCAGACT 1260
QY 1309 GTGGTTTCTGGGATGAGAGAGGGAATCATCTGAAATTTTGGCCCAATATGAAAT 1368
Db 1261 GTGGTTTCTGGGATGAGAGAGGGAATCATCTGAAATTTTGGCCCAATATGAAAT 1320
QY 1369 AGTGGTTTCTAAATGACAGCCCTTCTCTGAGAGATGAGTGTTCACACTGAAAA 1428
Db 1321 AGTGGTTTCTAAATGACAGCCCTTCTCTGAGAGATGAGTGTTCACACTGAAAA 1380
QY 1429 TGCAGCTATGATGAGTGAAGACAAAAGATCATGAGGCGATGAGTGAAGACAGC 1488
Db 1381 TGCAGCTATGATGAGTGAAGACAAAAGATCATGAGGCGATGAGTGAAGACAGC 1440
QY 1489 AGCTCTGATATGTTGGTCTCTACCTGTGTATAGTATAGTTCCTGGCCGCTGAA 1548
Db 1441 AGCTCTGATATGTTGGTCTCTACCTGTGTATAGTATAGTTCCTGGCCGCTGAA 1500
QY 1549 CGACATGAGGAGTGAAGAAACCTGTATTGCTCCAGAGACCCATATTGTGATGATA 1608
Db 1501 CGACATGAGGAGTGAAGAAACCTGTATTGCTCCAGAGACCCATATTGTGATGATA 1560
QY 1609 AAGGAAGGTGTTGCTGAGCATTATTCACCCACAGAGACTGACTTTTGACAGAGAC 1668
Db 1561 AAGGAAGGTGTTGCTGAGCATTATTCACCCACAGAGACTGACTTTTGACAGAGAC 1620
QY 1669 ATAGAGGTGAGCAATACAGATGCTGAGGAGCTGTACAAATTCCTTGTGGACTGAAT 1728
Db 1621 ATAGAGGTGAGCAATACAGATGCTGAGGAGCTGTACAAATTCCTTGTGGACTGAAT 1680
QY 1729 GGGCATTCAGTCCCTGCTGCGCAGACACACACATCATGATTGGAGGCTCAAGAGGG 1788
Db 1681 GGGCATTCAGTCCCTGCTGCGCAGACACACACATCATGATTGGAGGCTCAAGAGGG 1740
QY 1789 TATGAGCTAGGAGAGATGCTGAGTGAAGCATGCTTGAATCACTGACAGACACA 1848
Db 1741 TATGAGCTAGGAGAGATGCTGAGTGAAGCATGCTTGAATCACTGACAGACACA 1800
QY 1849 GACCCCTTGGGGAGTGTCTTCCATATATCACAAGACAAAGAGAGATTGGGAA 1908
Db 1801 GACCCCTTGGGGAGTGTCTTCCATATATCACAAGACAAAGAGAGATTGGGAA 1860
QY 1909 AGTACCTCAAAAGGCCAGACAGCTGG 1936
Db 1861 AGTACCTCAAAAGGCCAGACAGCTGG 1888

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RESULT 8

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US-09-957-187-82
; Sequence 82, Application US/09957187
; Publication No. US2003005451A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A.
; APPLICANT: Laroche, William
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FID REFERENCE: 15966-540 CIP
; CURRENT FILING DATE: US/09/957, 187
; PRIOR APPLICATION NUMBER: 60/123, 667
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 09/520, 781
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/234, 082
; PRIOR FILING DATE: 2000-09-20

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; PRIOR APPLICATION NUMBER: 60/233, 798
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/174, 485
; PRIOR FILING DATE: 2000-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1884)
US-09-957-187-82

Query Match 60.8%; Score 1881.6; DB 11; Length 1890;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1884; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 49 GGGCTGTTTCCAGAAATTCGAGCCAAATCAGTATTTCGCATGGCACTATACAAA 108
Db 1 GGATCCGGTTCACAGAGATTCGACCAATCAGTATTTCGCATGGCACTATACAAA 60
QY 109 CAGTATCCGGTGTGTTGGGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 168
Db 61 CAGTATCCGGTGTGTTGGGCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 169 GACATCCAGATGATTAATGATCAGAGGAAACCTCTACATTCCTGCTAGGACCATTT 228
Db 121 GACATCCAGATGATTAATGATCAGAGGAAACCTCTACATTCCTGCTAGGACCATTT 180
QY 229 TATACGTGATATAGACACATCAACAGGAGAAATTTATGACAAATACTGACA 288
Db 181 TATACGTGATATAGACACATCAACAGGAGAAATTTATGACAAATACTGACA 240
QY 289 TGGAAATCTAGACAGCGGATGTAGACACATGACGAATGAAGGAGAAACATAGAGAG 348
Db 241 TGGAAATCTAGACAGCGGATGTAGACACATGACGAATGAAGGAGAAACATAGAGAG 300
QY 349 TGGCAACAATTAATAAGTCTCTAAGAAAAAGTATGATGTTGTCTGTGA 408
Db 301 TGGCAACAATTAATAAGTCTCTAAGAAAAAGTATGATGTTGTCTGTGA 360
QY 409 ACTAATGCTTCAACCCCTTCTCTGAGAAATTAAGATGATATGATGAAACATTCGGG 468
Db 361 ACTAATGCTTCAACCCCTTCTCTGAGAAATTAAGATGATATGATGAAACATTCGGG 420
QY 469 GATGAATTCAGCGGATGCGCAGATGCCATATGATGCGCAAAACATGCAAGGTGCACTG 528
Db 421 GATGAATTCAGCGGATGCGCAGATGCCATATGATGCGCAAAACATGCAAGGTGCACTG 480
QY 529 TTTGAGATGAGAAACCTATCTACAGCCAGTGAATGATGCTTCTGCTTACGACAGTC 588
Db 481 TTTGAGATGAGAAACCTATCTACAGCCAGTGAATGATGCTTCTGCTTACGACAGTC 540
QY 589 ATTTACCGAGTCTTTGAGAAAGCCCTACCTCGCGAGCCGTCAGACAGATTCAAAATGG 648
Db 541 ATTTACCGAGTCTTTGAGAAAGCCCTACCTCGCGAGCCGTCAGACAGATTCAAAATGG 600
QY 649 TTGAAGAACAATCTTTGTCACAGCGGTGATTCGAGATTAATATCTACTTCTCTTC 708
Db 601 TTGAAGAACAATCTTTGTCACAGCGGTGATTCGAGATTAATATCTACTTCTCTTC 660
QY 709 AGGAAATAGCAGTGGATATACCAATGGAAGAGTATTTTCCCAAGAGTGGCTCAG 768
Db 661 AGGAAATAGCAGTGGATATACCAATGGAAGAGTATTTTCCCAAGAGTGGCTCAG 720
QY 769 GTTTTAAGATGATATGAGAGATCTCAAAAGATCTCGAGAAACAGAGGAGCTGCTTC 828
Db 721 GTTTTAAGATGATATGAGAGATCTCAAAAGATCTCGAGAAACAGAGGAGCTGCTTC 780
QY 829 CTGAAGGGCGCTTACGTCAGTTCCTGAGAGACTGCATTTTATTTCAACATCTC 888

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; Sequence 60, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

Query Match 18.3%; Score 565; DB 9; Length 1472;
Best Local Similarity 99.5%; Pred. No. 3,4e-166;
Matches 576; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2515 GCCCAGATGGCGCTGTGAGGACCCGCGCCACACTGAGTATTAAGACCATCAGGAACAT 2514
DB 13 GCCCAGATGGCGCTGTGAGGACCCGCGCCACACTGAGTATTAAGACCATCAGGAACAT 72
QY 2575 CTCGACGACGAAGATGCCACACCATGGGGTGAACCTTGTGAGAACCTGAGACGCTGCC 2634
DB 73 CTCGACGACGAAGATGCCACACCATGGGGTGAACCTTGTGAGAACCTGAGACGCTNNCC 132
QY 2635 CCCAAGTTCACAGCGGGAGGCGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCTCAGACC 2694
DB 133 CCCAAGTTCACAGCGGGAGGCGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCTCAGACC 192
QY 2695 GGCTAAGCAAGCGGCTGGAATGACACACTCTCTCCAGGAGGTTGACTATAAGAGG 2754
DB 193 GGCTAAGCAAGCGGCTGGAATGACACACTCTCTCCAGGAGGTTGACTATAAGAGG 252
QY 2755 AGTACCCCAAGAACTGCTCAGCAGAGAACCCAGGACCACTCTCAAAAGAAACAC 2814
DB 253 AGTACCCCAAGAACTGCTCAGCAGAGAACCCAGGACCACTCTCAAAAGAAACAC 311
QY 2815 ACTAAGTCTCCAAATTCCTCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 2874
DB 312 ACTAAGTCTCCAAATTCCTCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 371
QY 2875 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGACACACTCCGAGCTTCGGC 2934
DB 372 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGACACACTCCGAGCTTCGGC 431
QY 2935 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACACTGACAGAGGTG 2994
DB 432 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACACTGACAGAGGTG 491
QY 2995 GGGCTGAAGCGGTACGCGCTGTGTAAGCGGAGGTACCCCCCAACATCTTTGTCTCC 3054
DB 492 GGGCTGAAGCGGTACGCGCTGTGTAAGCGGAGGTACCCCCCAACATCTTTGTCTCC 551
QY 3055 CTTTCCATCCATGAAGCCCAATGATGCGTGTACATAA 3093
DB 552 CTTTCCATCCATGAAGCCCAATGATGCGTGTACATAA 590

US-09-925-299-60
; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

Query Match 18.3%; Score 565; DB 11; Length 1472;
Best Local Similarity 99.5%; Pred. No. 3,4e-166;
Matches 576; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2515 GCCCAGATGGCGCTGTGAGGACCCGCGCCACACTGAGTATTAAGACCATCAGGAACAT 2514
DB 13 GCCCAGATGGCGCTGTGAGGACCCGCGCCACACTGAGTATTAAGACCATCAGGAACAT 72
QY 2575 CTCGACGACGAAGATGCCACACCATGGGGTGAACCTTGTGAGAACCTGAGACGCTGCC 2634
DB 73 CTCGACGACGAAGATGCCACACCATGGGGTGAACCTTGTGAGAACCTGAGACGCTNNCC 132
QY 2635 CCCAAGTTCACAGCGGGAGGCGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCTCAGACC 2694
DB 133 CCCAAGTTCACAGCGGGAGGCGCTCCCTGGGTCGCCCGGAGAGCTCCCTGTCTCAGACC 192
QY 2695 GGCTAAGCAAGCGGCTGGAATGACACACTCTCTCCAGGAGGTTGACTATAAGAGG 2754
DB 193 GGCTAAGCAAGCGGCTGGAATGACACACTCTCTCCAGGAGGTTGACTATAAGAGG 252
QY 2755 AGTACCCCAAGAACTGCTCAGCAGAGAACCCAGGACCACTCTCAAAAGAAACAC 2814
DB 253 AGTACCCCAAGAACTGCTCAGCAGAGAACCCAGGACCACTCTCAAAAGAAACAC 311
QY 2815 ACTAAGTCTCCAAATTCCTCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 2874
DB 312 ACTAAGTCTCCAAATTCCTCTCAGCTCTCCAGAAACAGAGCTTTGGCAGGGAGACAC 371
QY 2875 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGACACACTCCGAGCTTCGGC 2934
DB 372 CCGCGCGCGCGCGCGAGAGGGTGGACTCCATCCAGGTGACACACTCCGAGCTTCGGC 431
QY 2935 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACACTGACAGAGGTG 2994
DB 432 CAGGCGGTGACTGTCTCGAGGACGCCAGCTTCAACGCTTACAACACTGACAGAGGTG 491
QY 2995 GGGCTGAAGCGGTACGCGCTGTGTAAGCGGAGGTACCCCCCAACATCTTTGTCTCC 3054
DB 492 GGGCTGAAGCGGTACGCGCTGTGTAAGCGGAGGTACCCCCCAACATCTTTGTCTCC 551
QY 3055 CTTTCCATCCATGAAGCCCAATGATGCGTGTACATAA 3093
DB 552 CTTTCCATCCATGAAGCCCAATGATGCGTGTACATAA 590


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1675 CBTGGCAATACAGATGCTGTCGGGGGACTG 1703
1743 GGGGGCCAGCACCTTCAGGCTTTAGGGGACTG 1771

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QY 73 GAGCCATCATGATTTCCATGCGCACTATACAAAACAGTATCCGGTGTGTGGGCCAC 132
DB 112 CCGCGCTTAGCGGTGGGCCCCAGGAGTACTGTAACACATATCCGGTGTGTGGGCCAGC 171
QY 133 AAGCCAGAGGAGAACACAC-----ACAGAGGACACAGGCTGGACATCCAGATGATATG 186
DB 172 GGGCCCGGAGCGCTGAGCCCGGAGAGGCTGAGAGCTCAACATCCAGAGCTCTG 231
QY 187 ATCATGAGAGGAGCCCTCATATGCTGCTAGGAGACATATTTATATCTGATATAGAC 246
DB 232 CGGCTCAACAGAGAGCTGTTACTTGGGAGACAGGAGACACTTACCGCTAGAGCTGGAG 291
QY 247 ACATCACACAGAGAGAAATTTATTTAGCAAAAACTGACATGAAATCTAGACAGCC 306
DB 292 CCCCCCAGTCCAGGAGGTGCGGTACACAGAGAGCTGACCTGGAGATCTTAACCCAGC 351
QY 307 GATGTAGACATGACAAATGAGAGGAGAAACATATAGATAGTCCCACTTATATAA 366
DB 352 GACATTAACGTGTGTGGATGAAAGGCAAAAGAGGAGGAGGTGTGCAAACTTCTGTAAG 411
QY 367 GTTCTTCTAAGAAAAAGATGATGATGATGTTGTGTGTGAACTATATGCTTCAACCT 426
DB 412 GTGCTGCTCTTGGGAGAGAGTCCAGCTCTTGTGTGTGTGCGGTTCCAAAGCTTCAACCG 471
QY 427 TCCGCAAGAACTATTAAGATGATACATTTGGAACCATTCGGGGATGAAATTCAGGGATG 486
DB 472 GTGTGCGCAACTACAGCATAGACACCTGAGCCGCTGAGAGCAACATGAGGGATG 531
QY 487 GCCAGATGCCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546
DB 532 GCCCGCTGCCGCTGAG 591
QY 547 TACTAGACCACTATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 606
DB 592 TTACAGACTCTGTTACAGACTTCTGAGCTGATGATGATGATGATGATGATGATGATG 651
QY 607 GAAAGCCCTACCTGCGGAG 666
DB 652 GACAGGCCACCTGCGGAG 711
QY 667 GTTCAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 726
DB 712 GTTCATGAGGTGAGAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 771
QY 727 TATAACACCATGAG 786
DB 772 TTTAACTAACCTGAG 831
QY 787 GAGAGAGCTCAAAAGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
DB 832 GGAAGCTTCCCGCGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 891
QY 847 TGCTAGTTCCTGAG 906
DB 892 TGCTGTGAG 951
QY 907 ATTCGATCAACAGGAG 966
DB 952 GTCAGAGCTCGGGGAG 1011
QY 967 CCGGAGTGTGAG 1026
DB 1012 CCGGAGTGTGAG 1071
QY 1027 TTCAAG 1086
DB 1072 TTCCAG 1131
QY 1087 AAGCCAG 1146
DB 1132 CGAGCCCGGAG 1185
QY 1147 GAGTTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1206

DB 1186 GCGTTCGAG 1245
QY 1207 CCGTCCATCTTCAACAG 1266
DB 1246 CCGTCCGAG 1305
QY 1267 ATTGAGTGCAG 1326
DB 1306 GTGCTGTGAG 1365
QY 1327 GAG 1380
DB 1366 GAGGCGGAG 1425
QY 1381 AATGACAG 1434
DB 1426 GAGCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1485
QY 1435 TATGATGAG 1494
DB 1486 GCGGCTGAG 1545
QY 1495 CTGATGATGAG 1554
DB 1546 CTGCTGAG 1605
QY 1555 GCGAG 1614
DB 1606 TCGGAG 1665
QY 1615 GGTGAG 1674
DB 1666 GCGT-----CTGATCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1722
QY 1675 GGTGAG 1703
DB 1723 GGGGAG 1751

RESULT 14
US-10-035-977-34
: Sequence 34, Application US/10035977
: Publication No. US20030134327A1
: GENERAL INFORMATION:
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pau, James
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P303081C10
: CURRENT APPLICATION NUMBER: US-10/035,977
: CURRENT FILING DATE: 2001-12-26
: PRIOR APPLICATION NUMBER: 60/085579
: PRIOR FILING DATE: 1998-05-15
: PRIOR APPLICATION NUMBER: 60/112514
: PRIOR FILING DATE: 1998-12-15
: PRIOR APPLICATION NUMBER: 60/113300
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: PRIOR APPLICATION NUMBER: 60/113430
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: PRIOR APPLICATION NUMBER: 60/114140

QY 487 GCCAGATGCCATATGATGCCAAACATGCCACCTGGACTGTTGAGATGAAACTA 546
DB 532 GCCCGCTGCCGTCGACGCCACAGCCCATGTGCTCCCTCTCTGAGCGGATGCTC 591
QY 547 TACTACGACAGTACGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 606
DB 592 TTCCAGCTTACTGTTACCGACTTCCATGACCATTTGATGCTGCTGCTGCTGCT 651
QY 607 GAAAGCCCTACCCCTGCGGACGCTGACGACGATTCAAATGTTGAAAGAACCTACTT 666
DB 652 GACAGGCCACCGCTGCGGACGCTGAAACATGACCCAGTGTCTCAAGAGCCCTACTT 711
QY 667 GTTACAGCCGCTGATTCAGGAGATTATCTACTTCTTCTTCAAGGAAATACAGTGA 726
DB 712 GTCCATGCGGTGAGTGGGACGACGATCTACTTCTTCTTCCGAGATTCGATGAG 771
QY 727 TATACACCATGGGAAAGTAGTTTCCCAAGAGTGGCTCAGTTTGTAAAGATATAG 786
DB 772 TTTCATACCTGCGGAGAGTGGTGTCCCGCTGGCCCGAGTGTCAAGAACGACGTG 831
QY 787 GAGAGATCTCAAAAGTCTGAGAACAGTGCAGTCTGCTGAAGGCGCGCTGAAC 846
DB 832 GAGAGCTTCCCGCGCTGCTGAGAACAGTGCAGTCTGCTGAAGGCGCGCTGAAC 891
QY 847 TGCTCAGTTCCTGAGACTCTCATTTTATTTCAACTTCTCCAGGCAATTACAGATGTG 906
DB 892 TGCTCTACCCGAGACTCCCATTTCTACTACAGTGTGCAAGGCTGCACGCGGTG 951
QY 907 ATTGCTATCAAGGCGCTGATGTGCTGCGCAAGTTTCTTACACCTTATACAGCATC 966
DB 952 GTCCAGCTCGGCGGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
QY 967 CTTGGGTCTGCACTCTGCTGCTATGACATGCTTGACATTCGACAGTGTGTTTACTGGAGA 1026
DB 1012 CTTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
QY 1027 TTCAAGGAAAGAGTCTCTGATTTCCACTGAGACACCATGTTCTGATGAACAGTCTC 1086
DB 1072 TTCCGAGAGCAAGATCCCGGAGTCCATCTGAGCGCGGTGCGGAGATCAGTGTCT 1131
QY 1087 AAGCCAGGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
DB 1132 CGACCCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
QY 1147 GAGTTCCTGATGATACCTGATTCATCAAGACGACCCGCTCATGATGAGGCAGTG 1206
DB 1186 GCTTGGCGGATGATCTCAACTTGTGAAGACCCACCTGATGAGAGGCGGTG 1245
QY 1207 CCGTCATCTTCAACAGGCAATGTTCTGAGAACATGTCAGATACCGCTTACCAA 1266
DB 1246 CCGTCTGCTGGGCGATGCGCTGATCTGCGGACCTGATGAGGCAACGCTGATCGA 1305
QY 1267 ATTGAGTGGACACAGCTGCTGCGCATATCAGATCACAAGTGTGTTTCTTGATCA 1326
DB 1306 GTGGCTGTGGACGTGGAGCGCGCTGCGGCAACAGACCGTGTCTTCTGCGGTCT 1365
QY 1327 GAGAGGGAATCATCTTGAAGTTT-----GGCCAGATAGGAATAGTGTCTTA 1380
DB 1366 GAGGCGGGGAGCGCTCAAGTTCTCTGCTGCGGCCAATGCAACCTCAGGACGCT 1425
QY 1381 AATGACAGCCTTTCTGAGAGAGATGATGTTTACAACCTCTGAAAATAGCAG-----C 1434
DB 1426 GGGCTCAAGTGTCTTCTGAGAGATTTGAGACCTACCGCGCGGACAGGTGTGGAGGCC 1485
QY 1435 TANGATGAGTGAAGACAAAGATATGAGGATGAGGCTGAGCAGAGCAGCTCT 1494
DB 1486 GCGGCTGAGGAGACAGGACGCGCTGCTGAGCTTGAAGCTGAGCAGCTTGGGGGGC 1545
QY 1495 CTGATGTGCTGCTCTACTCTGTGATTAAGSITCCCTTGGCCGCTGTAAGAGCAT 1554
DB 1546 CTGCTGCTGCTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1605
QY 1555 GCGAAGTGTAAAAAACCCTGATGCTCCAGAGACCATATGTGATGATGAAGGAA 1614

DB 1606 TCGGGGTGTATGAGAACTGTATCGGACGTCAGACCCCTACTCGGGTGGCCCCGAC 1665
QY 1615 GGTGTGCTGCGACGCAATTTATACCCACAGCAGAGCTGATTTGAGCAGACATAGAG 1674
DB 1666 GGTCT---CTGCACTTCTCTACGCCCGGCGCACAGAGCGGCTTTGAGCAGAGATGCTC 1722
QY 1675 CGTGGCAATACGATGCTGCGGAGCTG 1703
DB 1723 GGGGCGACACCTCAGGCTTAGGGGAGCTG 1751

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